

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 121831

TO: Jon Ashen

Location: REM-2B02/2C18

Art Unit: 1635

Friday, May 14, 2004

Case Serial Number: 09/673994

From: Toby Port

Location: Biotech-Chem Library

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Ashen,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port



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GenCore version 5.1.6
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May 13, 2004, 10:04:10; Search time 1380 Seconds (without alignments) 11842.622 Million cell updates/sec model - nucleic search, using sw OM nucleic Run on:

US-09-673-994A-7 3847 Title: Perfect score:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

3373863 segs, 2124099041 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

N Geneseq 29Jan04:*

1: genesequ1980s:*
2: genesequ1990s:*
4: genesequ2001as:*
5: genesequ2001bs:*
6: genesequ2001bs:*
8: genesequ2003bs:*
9: genesequ2003bs:* geneseqn2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | 0 0 0 0 | % Query Match | * Query Match Length | 03 | COMPARATOR | Description |
|--------|------------------|---------------------|----------------------------|-----|------------|--------------------|
| | 2001 | ייים ביייי | TO STORY | 3 ! | | - |
| 1 | 3836 | 99.7 | 3847 | ო | AAZ35044 | Mouse |
| N | 2628.4 | 68.3 | 2651 | m | AAZ35053 | Mouse |
| m | 1988.4 | 7.75 | 2336 | ო | AAZ35052 | Mouse |
| 4 | 1671.8 | 43.5 | 1696 | 7 | ACC83475 | _ |
| Ŋ | 1504.4 | 39.1 | 1860 | 7 | ACC83474 | Acc83474 Rat chond |
| Φ | 1498 | | 1975 | ហ | ABA82987 | Human |
| 7 | 1392 | 36.2 | 1855 | 7 | ACC83473 | Acc83473 Human cho |
| 00 | 7 | 35.5 | 1996 | m | AAA93131 | Human |
| σ | \sim | 31.7 | 1488 | 4 | AA159942 | Aai59942 Human pol |
| 10 | _ | 31.1 | 9266 | 4 | AAK85394 | Human |
| 11 | 1195 | 31.1 | 9266 | 4 | AAL04937 | Aal04937 Human rep |
| 12 | 1195 | 31.1 | 9266 | 4 | ABL97831 | Ab197831 Human tes |
| C) 13 | 1195 | 31.1 | 9266 | w | ABA15877 | Aba15877 Human ner |
| ٦, | S | 29.0 | 1456 | 7 | ADA53558 | Human |
|) | œ | 21.2 | 1558 | 4 | AAI58156 | Aai58156 Human pol |
| 16 | 815.2 | 21.2 | 1558 | œ | ADB48122 | Novel |
| 17 | 615.8 | 16.0 | 1824 | N | AAT91793 | FINI3 |
| C) 18 | 576.8 | w | 581 | 'n | AAZ35050 | Aaz35050 Mouse EST |
| 7 19 | 528.4 | 13.7 | 851 | 7 | AAX00648 | Aax00648 Human sec |
| 20 | 511.4 | 13.3 | 559 | Ŋ | AAH97867 | Aah97867 Murine 7- |
| 21 | 49 | 12.9 | 509 | ო | AAZ35045 | Aaz35045 Mouse EST |
| 22 | 485.8 | 12.6 | 500 | M | AAZ35046 | Ģ |
| 23 | 84 | 12.6 | 562 | Ŋ | AAH97866 | Aah97866 Murine 7- |
| | ٠ | i | | | | |

| Mouse | Human | Aal04938 Human rep | | | | | œ | -1 | σ | | | Aai97820 Human neu | Human | Human | Human | Aaz35049 Mouse EST | Aak63629 Human imm | Adc99137 Human KPP | Aac77184 Human ORF | Human | |
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| AAZ35051 | AAK85395 | AAL04938 | ABL97832 | ABA15878 | AAH97868 | AAH97870 | AAZ35048 | ABL01567 | AAH97869 | ABK62729 | ABQ78852 | AAI97820 | AAF22730 | ADC38710 | ACC51151 | AAZ35049 | AAK63629 | ADC99137 | AAC77184 | AAH11322 | |
| 586 3 | 6271 4 | 6271 4 | 6271 4 | 6271 5 | 605 5 | 578 5 | 446 3 | 1573 6 | 616 5 | 496 6 | 1435 6 | 706 4 | 809 4 | 1934 9 | 535 7 | 441 3 | 502 4 | 2167 9 | 727 3 | 525 4 | |
| 11.7 | 11.6 | 11.6 | 11.6 | 11.6 | 11.5 | 11.5 | 11.5 | 11.4 | 11.3 | 10.4 | 10.0 | 10.0 | 6.6 | 8.6 | 5.5 | 0.6 | 8.7 | 0.8 | 7.6 | 6.3 | |
| 450.2 | 444.8 | 444.8 | 444.8 | 444.8 | 443.6 | 442.2 | 441.8 | 437.8 | 434.8 | 399.2 | 385.6 | 383.6 | 380 | 376 | 364.4 | 346.8 | 336.6 | 306.4 | 294 | 240.8 | |
| c 52 | 26 | 27 | 28 | | | 31 | | | 34 | 323 | 36 | C 37 | 38 | 39 | 40 | 4 | 4 4 | 43 | 44 | c 45 | |
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ALIGNMENTS

CNREB-2; CNRE binding factor; transcription factor; mouse; renin; negative regulatory element; cardiovascular disease; hypertension; congestive heart failure; diagnosis; therapy; ss. Location/Qualifiers 1198. .3489 /*tag= a 3809. .3814 /*tag= b AAZ35044 standard; cDNA; 3847 BP Mouse CNREB-2 cDNA clone KND42. 98US-0082997P. 99WO-US008502 (first entry) 24-APR-1998; Mus musculus WO9955343-A1 23-APR-1999; 28-FEB-2000 polyA_signal 04-NOV-1999 AAZ35044; RESULT 1 Key

Tamura (BGHM) BRIGHAM & WOMENS HOSPITAL INC. Dzau VJ, Chen YE, Horiuchi M, WPI; 2000-062002/05. P-PSDB; AAY32375. A new regulatory element binding factor used to treat an adverse cardiovascular condition.

Claim 1; Page 77-79; 57pp; English.

This is the nucleotide sequence of cDNA clone KND42 encoding mouse negative regulatory element binding transcription factor CNREB-2. KND42 was obtained using yeast one-hybrid cloning and mouse kidney cDNA library screening. CNREB-2 binds to the 5' flanking region of the renin gene and

modulates expression of the gene. 2 Other isoforms (see AAX32376-77) of CNREB-2 have been identified, the shortest isoform showing strongest bindings activity to the CNRE of the renin promoter. CNREB-2 shares no significant homology to any other known gene or protein. It is a novel zinc finger transcription factor. Expression vectors, isolated nucleic acid molecules and CNREB-2 polypeptides are claimed. The invention also relates to CNREB-1 polymetheotides (see AAZ35040-43), polypeptides (see AAX32374) and inhibitors, and their use in claimed methods for decreasing or increasing remin expression, and for determining the level of CNREB-1 susceptibility to development of a remin-angiotensin system mediated disorder 8888888888888888888

Sequence 3847 BP; 805 A; 1008 C; 1171 G; 852 T; 0 U; 11 Other;

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720 780 CTCTCTTGGGCTCATCGACTATCGGTTCTGTGCCTGTGCTTGTGTTGGAGGGAAG 840 120 180 180 240 240 300 300 360 360 420 420 480 480 540 540 600 600 999 9 720 780 120 9 9 GCCCCCCACCCCCCCACGCGGCAGCCTGGAGGCTCTGCTGTCCTTAAGCCTCTTA AGAAATTNACNGTTTTTTTTTTTTGTGATAACTTGCCCATTCTTTGTGTCCTGCTTTCTTG 301 TATTAGCAAGGACAAGCTTTCTTGTGTACTTTGGTTCAAACCCCATGGCTAAACTGCCT <u> AGGCAGAGAGTGGCAAGAGGAAACTGGAGGAGGCACTGTCCACGGAGGGGGCTGAAGACA</u> CCGGCAACACTGACAAAAAGAAGGCCAAGAGGATTAGTGGTCAACCGGACCCTGCCCAT <u> AGCAGTGGGTATGAGGTGTGCAGGGGGCTGGGTGGCTTTCCTCCAGCCCATTACAAAGAGG</u> AGCAGTGGGGTATGAGGTGTGCAGGGGGGGGGGGGTTTTCCTCAGCCCATTACAAAGAGG GCCCCCCCCCCCCCCCACGCCAGGCCTGGGAGGCTCTGCTGTCCTTAAGCCTCCTTA ceacerreracarreracearcasearcasecercarcasearcasearcasecerce TTAGTGACTTTGATTAAAANGGNGGTTNTTTCTTCATTTCCCAGATGTAGCCTGGGCTTC TTAGTGACTTTGATTAAAANGGNGGTTNTTTCTTCATTTTCCCAGATGTAGCCTGGGCTTC AGAAATTNACNGTTTTTTTTTTTGTGATAACTTGCCCATTCTTTGTGTCCTGCTTTCTTG TATTAGCAAGGACAAGCTTTCTTGTGGTACTTTGGTTCAAACCCCATGGCTAAACTGCCT TAACCTTTTTGTAGCTGCTGGTGATCAGTGCCTGGCGCCAGACACTTCTGGGGATGGTACAG GGTGTGACAACATGACGTGCATCATTTTTTTTCAAGCCCCGAAACACAGTAGAGCTTC GGTGTGACAACATGACGTGCATCATTTGTTTCAAGCCCCGAAACACAGTAGAGCTTC **AGGCAGAGAGTGGCAAGAGAAACTGGAGGAGGCACTGTCCACGGAGGGGGCTGAAGACA** CCGGCAACAGTGACAAAAGAAGGCCAAGAGGGATTAGTGGTCAACCGGACCCTGCCCAT GIGGACTGITITCIGAGCCCITGGACCCGAGACTGAGTTITGICCTTGICCTTAGCCTT gradacterrirergadecerrigaaceceagaeregaerrirerecerrirageerr GGAGGTTGTAGACTTTATTCAATCAAAGATCAGTCAACGTGATGAAAACGGGGAGCTTCG GITAITGICAICCAITGIGGAAGAGGIGAGICTAAAGITGGGAGGGAGGNGNITGGINIA AAACAGANAATTTTTTTTGAGATGTGAGCAGGGGGGGGGTTAGATTCACTGAANACAA Gaps ô DB 3; Length 3847; Indels ö 99.7%; Scor. 100.0%; Pred. No. v. Best Local Similarity 100. Matches 3847; Conservative 421 481 541 601 601 199 661 721 781 61 19 121 181 181 241 241 301 361 421 481 541 721 Query Match

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|------------|------|--|--------------|
| K | 841 | GACTGGTAGTTCTGTGTTTTTACTCTGTGAACACTTTATTTA | 006 |
| qc | 841 | dacidenaciictoaiiiinacicididaacaciinarriaaeeacarictirriaire | 006 |
| à | 901 | GCGCTCTGTGACCCCTAGCCGCTTGCACCCCGCTCTCTGTTGTACACTTTCAAGCAACAC | 096 |
| ą | 901 | GGGGCTCTGTGACCCCTAGCGCCTTGCACCCGCTCTGTTGTACACTTTCAAGCAACAC | 096 |
| À 1 | 961 | TITICAGACTAAAGGCCAAACAAAAGCTAATCGTGCTCATAGTGTCATGCTTTACTCTC | 1020 |
| g 3 | 961 | TITITCAGACTAAAGGCCAAACAAAAGCTAATCGTGCTCATAGTGTCATGCTTTACTCTC ABBACACAAAAAAAAAAAAAAAAAAAAA | |
| ₹ 8 | 1021 | CTACCCTGGCCCCATAIGTGGTGGCGCGCTGTTGCTGTGTTGTTGTTGTTGTTGTTG | 1080 |
| λά | 1081 | TCTGGAGAGGGGGGAGTGAATGTGGAGCAGGAGCTGGGAGTCTTAACTCCTGAGTAAGCA | 1140 |
| q | 1081 | tchggagagagagagangaangnggagcagcnggagcnggagcnnaactccngagnaaca | 1140 |
| k a | 1141 | 141 GCCGCCTGGARGGCCATCCTGGGCTGTTCGGCTTCAGGACGACTTCCTAGTTCGTTGTTTGT | 1200 |
| à | 1201 | GAGGGGGAGGTACCACCTTCCTGGTTGGCTGGGTTAGGCTTAGGCTTAGGTTA | 1260 |
| 셤 | 1201 | GAGGGGGCAGGGTACCACCTTCCTGGTTGGCTTGGGTTACGCGTCCAGCTTCTGATT | 1260 |
| Kari | 1261 | GGTTGGCTAGCAGCGCATCACAATCACTTCCTGGTCATGCTGCGACTGCGCTCCGGTTGT | 1320 |
| g | 1261 | GGTTGGCTAGCAGCGCATCACAATCACTTCCTGGTCATGCTGCGACTGCGCTCCGGTTGT | 1320 |
| λ | 1321 | ACAGCCCATGAACTACGCATCCCGTGTTGCTCTGCGGTGGCGGAAGCGGAAGCGGGTACG | 1380 |
| ନ୍ଧ | 1321 | ACAGCCCATGAACTACGCATCCCGTGTTGCTCTGCGGTGGCGGAAGCGGAAGCGGGTACG | 1380 |
| કે ક | 1381 | GAGGTACCAGCTGGTCTTCGGAGGGGGGGTAGGGGGTTCCATGAATGGAATGGGAGCGGCGGC | 1440 |
| 3 2 | 1441 | GGGGGGACTGAGCTGAATTCCGGGGGCCGGGGCTGGCTCCCCGGGGCCCCCCCC | 1500 |
| ; A | 1441 | GECGGGGAGTGCTGAGCTGGATTCCGGGGCCGGGGCAGGGGCTGCCCAGGGCCCGCACC | 1500 |
| ò | 1501 | GTGTATGGGGGGGGCGGATCCTAAGAGCAAGACCGACGGCAGGGCCGAAACTGGGA | 1560 |
| qq | 1501 | GIGIATIGGGGCGGTTCGTGGATCCTAAGAGCAACGGACGGCAGGCCGAACTGGGA | 1560 |
| <i>\</i> 5 | 1561 | GGGGCGGGGGCCGGGGGCCCGGAGGCGCGTCGGGCCTGGAGCCGGTCACGATGCC | 1620 |
| 90 | 1561 | degecededededectededecedededededededededede | 1620 |
| ò | 1621 | CCGAAAGAAAGCAAAGCCATCCACAGCCCGTGAAATGCGAGGGGGTCAAAGGTCAGGGGTC | 1680 |
| DP DP | 1621 | CCGAAGGAAGCAAAGCCATCCACAGGCCCGTGAAATGCGAGGGGGTCAAAGGTCAGGGGTCA | 1680 |
| ά | 1681 | AGGGGCCTTGAGCCGGGAGGAACAGGGGTGGGGTCAGTAGAGTGGGCTCAGGTG | 1740 |
| Q O | 1681 | AGGGGCCTTGAGCCGGGAGGAGCAGGGTGGGGTCAGTAGAGTGGGCTCAGGTCAGGGTG | 1740 |
| දු ද | 1741 | GAGGGGACTCCTCAGGGTTAGGGGCGGATGATCTGGGATCTTCGCTCCTTACCAGGTA | 1800 |
| Q Q | 1741 | GAGGGGACICCICAGGGITAGGGGGGATGAICIGGGATICTICGCICCITACCAGAGA | 9 1 |
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| S 6 | 1861 | GTTCGGATTATGGCTACTGCTTGGGAGGGAAATTCCACAAAGGCACCTCCCCTCTTTAGGGAGGG | 1920 |
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Mus musculus

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                                                                                                                                                            GGTCAGGGGCCTTGAGCCGGGAGGAACAGGGGTGGGGGTCAGTAGAGTGGGCTCAGGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           961 GAGTGAAGTTGAGGAACCAGCCAGGGGTCCAGGGGAGGCCAGGGGTGAGGAGGCCAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1021 AGCCTGTCAGCTGTGTGGGGGGCCGACAGGTGAGGGGCCGTGTTGTGGGGGCCAGGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1261 CACCCATACTGGCGAGAAGCCCTACCGCTGTCCCCACTGCCCTTTGCCTGCAGCGCCT
                                                                                                                                                                                                                                                                                        GGTGGAGGGGACTCCTCAGGGTTAGGGGCGGATGATCTTCGCATCTTCCCTTACCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGGTTCGGATTATGGTACTGCTTGGGAGGGAGAGATTCCACAAAGCACCCCCCTCTTT
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CACCGTGTATGGGGGCGGTTCGTGGATCCTAAGAGCAAGGACCGACGGCAGGGCCGAACT
                 CACCGTGTATGGGGGGGGGTTCGTGGATCCTAAGAGCAAGGACGCCGACGGCGACGGCCGAAGGACC
                                                                      TGCCCCGAAGGAAGCCAAAGCCATCCACAGCCCGTGAAATGCGAGGGGGGTCAAAGGTCAGG
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     therapy;
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     failure; diagnosis;
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674. .2293
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P-PSDB; AAY32377.
     congestive heart
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This is the nucleotide sequence of a cDNA clone encoding mouse negative regulatory element binding transcription factor 2 (CNREB-2) short isoform capulatory element binding transcription factor 2 (CNREB-2) short isoform as contained using yeast one-hybrid cloning and mouse kidney cDNA library screening. CNREB-2 binds to the 5' flanking region of the remin gene and modulates expression of the gene. 2 Other isoforms (see AAY32377) of CNREB-2 have been identified, the short isoform showing strongest binding activity to the CNRE of the remin contain. It is a novel zinc finger transcription factor. Expression or vectors, isoform, a novel zinc finger transcription factor. Expression or protein. It is a novel zinc finger transcription factor. Expression or vectors, isoform also relates to CNREB-1 polymotlectides (see AAX35040-43), polypeptides (see AAY32374) and inhibitors, and their use in claimed methods for decreasing or increasing remin expression, and for determining the level of CNREB-1 expression, an increase in expression being indicative of an increase susceptibility to development of a remin angiotensin system mediated disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNREB-2S, CNRE binding factor; transcription factor; mouse; renin; negative regulatory element; cardiovascular disease; hypertension; congestive heart failure; diagnosis; therapy; ss.
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Czf-1

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The present sequence is that of a contig containing most of the murine Czf-1 coding sequence, lacking only the 5' portion which codes for the Neterinius of Czf-1 protein. The contig was obtained by screening mouse expressed sequence tag sequences using rat Czf-1 protein as a sequence probe. Czf-1 protein as a sequence probe. Czf-1 is expressed in a variety of tissue types, particularly osteoblasts and chondrocytes. It is expressed in the nuclei of hypertrophic chondrocytes of the growth plate, and exhibits an alternate expression and intracellular localisation pattern in cells expressing high, i.e. constitutively active, levels of fibroblast growth factor receptor (FGGR). It is up-regulated in osteoarthritic cartilage tissue and serves as a marker for osteoarthritis. Czf-1 has been found in rats, mice and humans. Sequence identity for nuclectide and amino acid sequences is above 85%. Czf-1 polynucleotides, polypeptides and serves as the characterisation, diagnosis and treatment of FGRR-related and skeletal diseases and disorders, such as ceteoarthritis, rheumatoid arthritis, and cartilage related diseases
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                                                                                             New chondrocyte-derived zinc finger polypeptides and encoding polynucleotides, useful for detecting, diagnosing and treating C protein-related diseases, such as osteoarthritis and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
43.5%; Score 1671.8; DB 7; Length 1696;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1687; Conservative 0; Mismatches 8; Indels 1;
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               Blumenstein
                                            WPI; 2003-457599/43.
P-PSDB; ABR42914.
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/note= "No start codon"
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3. .1355
/*tag= a
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The present sequence is that of CDNA was isolated from a glioma CDNA protein, designated Czf-1. The CDNA was isolated from a glioma CDNA ilbrary using a probe from the 3' end of the CZf-1 gene. CZf-1 is expressed in a variety of tissue types, particularly osteoblasts and chondrocytes. It is expressed in the nuclei of hypertrophic chondrocytes of the growth plate, and exhibits an alternate expression and intracellular localisation pattern in cells expressing high, i.e. constitutively active, levels of fibroblast growth factor receptor (FGFR). It is up-regulated in osteoarthritic cartilage tissue and serves as a marker for osteoarthritis. Czf-1 has been found in rats, mice and humans. Sequence identity for nucleotide and anino acid sequences is above 85%. Czf-1 polymucleotides, polypeptides and antibodies can be used in the characterisation, diagnosis and treatment of FGFR-related and skeletal diseases and discasses.
1621 AACTGGTTGGGAGCTGCCCAGCCTTTTACTGTTTTAACTTATTTCAGTGCTTTATAATAA 1680
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                                                                                                                                                                                                                                                                                                                                     Rat; Czf-1; chondrocyte; zinc finger; osteopathic; antiarthritic; antirheumatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New chondrocyte-derived zinc finger polypeptides and encoding polymucleotides, useful for detecting, diagnosing and treating of protein-related diseases, such as osteoarthritis and rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                   Rat chondrocyte-derived zinc finger protein Czf-1 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Rat Czf-1"
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176. .1801
/*tag= a
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                                      3814 AGGAAACACTAACAGA 3829
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PT associated with altered activity and expression of TRFX, and to screen XX XX SS Claim 11; Page 261; 327pp; English.

CC Claim 11; Page 261; 327pp; English.

CC factor. The transcription factor and its coding sequence are useful in the diagnosis treatment and prevention of diseases associated with altered expression of the transcription factor e.g. cell proliferative, cc autoimmune/inflammatory, neurological and developmental disorders. A number of specific disorders/diseases are given in the specification, including: arteriosclerosis, circles, hopstitis, cancers, AIDS.

CC allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout, Grave's disease, multiple sclerosis, osteoarthritis, panceative cc altergies, theumatoid arthritis, systemic lupus erythematosus, ulcerative cc psoriasis, theumatoid arthritis, systemic lupus erythematosus, ulcerative cc colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's disease, stroke, and viral, bacterial, fungal and protozoal infections XX Sequence 1975 BP; 396 A; 625 C; 612 G; 342 T; 0 U; 0 Other;
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| ú | | 2036 | 2096 | 2156 325 | 2216 385 | 2276 | 2336 | 2396 | 2456 625 | 2516 685 | 2576 745 | 2636 |
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| , 1 | GATTT GATTT GATTT | GGCCA GGCAA | AGACC - - - - AGGCC | TGGACTTCCCTATGGGCTGAGTGACGACGAGTCTGGGGGCGCCGCGCGCACTAAGTGCGGA | 20000 | AGCTGTCAGCTGTGTGTGGGGGGCCCAACAGTGAGGGGCCGTGTTGTGGGGGCGGAGGGCGGGGGGGG | Tregr | CCGTT | CCGCTGTGGCCCCTGCCCATACGCNTCAGCCCAGTTCGTCAACCTGACGCGACATACCCG | CACCATACTGGCGAGAAGCCCTACCGTTGTCCCCACTGCCCCTTTGCCTGCAGAGCTT CALL | GGGCAACCTGAGGCGGCATCAGCGCACCACACAGGGCCTCCCACTCCTCCCTGCCCAAC | CTGTGGCTTTCGATGCTGTCCACGACCAACCCGGCCTCCCAGTCCCACAGAGCAGGA |
| 5 2 3 | AGAGC | GTGAC GCGAC | | TAAGT | 60000 | CAGGA | 360601 | agaag agaag | GACAT | 36CAGO | 200199 | CAGAG |
| Length 197 | GTTGG | TGAAG GGAAG | 11CAGG | 000 CO | TGAGA TGAGA | 770000 | SCTG1 | 00000000000000000000000000000000000000 | GACGO | 77GCC | 11001 11001 11001 | |
| Length | 7. T.G.T. | AGAGGA AGAGGA | AGACTO | 399000 | 24GGGG | rerre | ATGCCC ATGCCC | ACACA | PACCI | | CCCCAC | rcccac |
| DB 5; | AGTGGATACTAAGATTCCTTCGACGAAGGTCCTGGGGCCCTGGTGTTCGAGAGTTTTAGACGATTTTAGACGATTTTAGACGATTTTAGACGATTTTAGACGATTTAGACGATTTAGACGATTTTAGACGATTTTAGACGATTTTAGACGACTCTTAGAAGGACCCTGGATTTAGAAGACTCCTCGAAGGACCCGGGGCCCTGGTATTGGAAGAGTATTAGAAGAACTATTAGAAGAACTATTAGAAGAACTAGATTTAGAAGAACTATTAGAAGAACTATTAGAAGAACTATTAGAAGAACTATTAGAAGAACTATTAGAAGAACTATTAGAAGAACTATTAGAAGAACTATTAGAAGAACTATTAGAAGAACTATTAGAAGAACTAATTAGAAACTAATTAGAAACTAATTAGAAGAACTAATTAGAAGAACTAATTAGAAGAACTAATTAGAAACTAATTAGAAACTAATTAGAAGAACTAATTAGAAACTAATTAGAAAAAAAA | gctactaggccaagatctggagtttgaagggaaggaagga | CAACGACCAGCTCATGGGCTTTGAGAGACTCTGAAGGAGACTCTCAGGGGGCCAGACC | 99999999999999999999999999999999999999 | ABOTGAAGTTGAGGAACCAGGGGTCCAGGGGAGGCCAGGGGTGAGAGGCCAGGGCCC | 000000 | gggiggggcccccccccccccccccccccccccccccc | GTCCCACTACTCGAGCCACTGAAGCGGCACATGCAGACACACAGCGGGGAGAAGCCGTT | TTCGT | CACTG | 00000 | |
| | GTCCT GACCC | AGGAA AGGAA | ACTCT ACTCG | AGTCT AGTCT | CAGGG | GTGAG GTGAG | TACTG TACTG | ACATG | CCCAG | GTCCC | ACACA | CAACO |
| Score 1498; I Pred. No. 0; | CGAAG CGAAG | TGAAG TGAGG | GAGAG GAGAG | CGACG | 96970 - - - 96970 | GACAG | ACGGT ACGGC | | NTCAG | CCGTT | CACCO | ACGAC |
| Score Pred. | TTCG. | CAGTT | TTTGA | AGTGA | 600A | | 00000 | CTGAA | TACGO TACGO | CCCTP | CAGCO | 790100 1-1-040 |
| 38.9%; | PATTCC | ATCTG | 11666 | 366CTG | ayacca | 191199 | 00000 00000 00000 | AGCCAC | 190007 | BAGAAC | 1966CA 1000CA 1960CA | 16C163 |
| 4 | TGAAC | SCCAAC CCAGC | AGCTC | CTATO | TTGAG | AGCTGT | 00000 100000 1000000000000000000000000 | ACTCG/ | 30000 | 011660 011660 011660 011660 | rgagg | TTCGA. |
| larity | SGATAC SGATAC | ACTAGG | GACC | ACTTCC GCTTCC | TGAAG | 0.1610 | 1999 | CCACT | CTGTG | CCACA | CAACC | 1466CT |
| Simil | 7 AGTO 6 AGTO | | | | | | | - | | r 10 | | |
| Query Match Best Local Similarity | 1917 | 1977 | 2037 | 2097 | 326 | 386 | 2277 | 2337 | 2397 | 2457 | 2517 | 2577 |
| Query Best 1 | | | | | | | | | | | | |

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| S G | 2757 G | 157 CTTGTGTGGAACTGGATCCGAACCACTGCCAGAGCTACTGTTCCCTTGGACCTGCCGGGG 2816 |
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| දු පු | 2877 C | AA 293 |
| X | 2937 | 28 299 |
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| දු දු | 2997 0 | CATGAAGACTCACAGTGGTGAGAAACCCTTCCGCTGTGCCCGCTGTCCATACGCCTCTG 3056 |
| ð í | 3057 I | 16 31 C |
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| දු යු | 3117 0 | CCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCAACCTCAAGGTCATGGTCGCATCCA 3176 |
| λò | 3177 0 | ACTACAGCTGCAACCAGAGTATGAA 323 |
| qq | 1346 | sagcardaa 140 |
| , S | 37 | PACCIGGG 329 |
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The present sequence is that of CDNA encoding a novel human zinc finger protein, designated Czf-1. Czf-1 is expressed in a variety of tissue nuclei, designated Czf-1. Czf-1 is expressed in a variety of tissue nuclei by particularly offerbolasts and chondrocytes. It is expressed in the nuclei of hypertrophic chondrocytes of the growth plate, and exhibits an alternate expression and intracellular localisation pattern in cells alternate expression and intracellular localisation pattern in cells factor receptor (FGFR). It is up-regulated in osteoarthritic cartilage tissue and serves as a marker for osteoarthritis. Czf-1 has been found in rats, mice and humans. Sequence identity for nucleotide and amino acid sequences is above 85%. The human gene maps to chromosome 2p22-23. Czf-1 polynucleotides, polypeptides and antibodies can be used in the disractisation, diagnosis and treatment of FGFR-related and skeletal diseases and disorders, such as osteoarthritis, rheumatoid arthritis, and cartilage related diseases 1909 GCCTCCCACCTGTTTATTTAACTTATTTTCAGTGCTTTATAATAAAGGAAACACTAACAAA 1968 GCCTTTTAC----TGTTTTAACTTATTTCAGTGCTTTAATAATAAAGGAAACACTAAACAGA Czf-1 Human, Czf-1; chondrocyte; zinc finger; osteopathic; antiarthritic; antirheumatic; chromosome 2p22-23; gene; ss. New chondrocyte-derived zinc finger polypeptides and encoding polymuclectides, useful for detecting, diagnosing and treating (protein-related diseases, such as osteoarthritis and rheumatoid arthritis. Sequence 1855 BP; 344 A; 590 C; 619 G; 302 T; 0 U; 0 Other; Human chondrocyte-derived zinc finger protein Czf-1 cDNA /product= "Human Czf-1" Location/Qualifiers 171. .1796 /*tag= a ACC83473 standard; cDNA; 1855 BP. Yayon A, Blumenstein S, Harari Claim 12; Fig 1; 64pp; English. 20-NOV-2002; 2002WO-IL000925 20-NOV-2001; 2001US-0331626P (PROC-) PROCHON BIOTECH LTD (first entry) 3830 AAAAAA 3836 1969 AAAAAA 1975 WPI; 2003-457599/43. P-PSDB; ABR42912. WO2003044159-A2 Homo sapiens 08-SEP-2003 30-MAY-2003 3774 1849 RESULT 7 ACC83473 g δ ò

DB 7; Length 1855;

1392; No. 0;

Score Pred.

36.2%; 92.6%;

Query Match Best Local Similarity

2876 2816 1123 1003 2756 1063 1244 AGGCTTTGCCTGTAGCCTCTGCCCCTTTGCCACTATCCCAACCACCTGGCCGGCA 1303 2036 2096 2156 2216 2276 2336 2396 2456 2516 2576 2636 2696 ô 643 703 823 883 943 523 283 403 463 CCGCTGTGGCCGCTGCCCATACGCNTCAGCCCAGTTCGTCAACCTGACGCGACATACCCG 944 GGGGGGGGGCCCGGGGGACCTGAAGATCCTCCCTTCCAGATTGAGCCTCCATGT 1004 GCCACCAGGTGCCAGTTTCCTGCCAGACTGTGGGCAGCTGCGGGGTGAAGGGGAGGG AGGCTTTGCCTGTAGTTTATGCCCCTTTGCCACTCACTACCCCCACCACCACCTCGGCTCGGCA CTCTGCGGGACTGGATCAGAACCACTGCCAGAGCTGCTATTCCCTTGGACCTGCCGGG CACCCATACTGGCGAGAAGCCCTACCGTTGTCCCCCACTGCCCCTTTGCCTGCAGCAGCCT GGGCAACCTGAGGCGGCATCAGCGCACCCACACAGGGCCTCCCCACTCCCTGCCCAAC 884 Créréctrececrécrécrécrécaceacecegecreceagecres Artifilities GCCACCAGGTGCCAGTTTCCTGCCAGACTGTGGGCAGCTGCGGGGTGAAGGGGGAGAG CITGIGIGGAACTGGAACCACTGCCAGAGCTACTGTTCCCTTGGACCTGCCGGGG CTGTGGACAGGAACTGGAGGAGGAGGCAGCAGCTGGGAGCTGCCATGTGTGGGCG 2877 CTGCATGCGAGGAGGCTGGAGGGTTGCCACTGGGGGACCCCAGGGCCCTGGTGACAA 344 CAGTGACCTCATGGGCTTCGAGAGACTCGGAAGGAGACTCTCTGGGGGCCAGGCC 2217 AGCCTGTCACCTGTGTGGGGGGCCGACAGTGAGGGGCCGTGTTGTGGGGGCAGGAGGGCG GGGGACAATGCCCCGACGATCAGAAATGCGCTGATCCTGCCAGACTTGAGTCTTCATGT 1917 AGTGGATACTGAAGATTCCTTCGACGAAGGTCCTGGGGCCCTGGTGTTGGAGGCGATTT 1977 GCTACTAGGCCAAGATCTGGAGTTTGAAGAGGAAGAGAGGAAGAGGATGAAGGTGACGGCCA 2097 IGGACTICCCIAIGGGCIGAGIGACGACGAGICIGGGGCGGCCGCGCACIAAGIGCGGA GGGTGGGGGCCCCCTGCCCCCACGTTACTGTACTCATGCCGGCTGTGCGCTTTTCGT CTGTGGCTTTCGATGCTGTGCTCCACGACCAACCCGGCCTCCCAGTCCCACAGAGCAGGA 224 AGTGGATACTGAAGACTCCCTCGACGAAGGACCCGGGGGCCCTGGTATTGGAGAGTGATTT CAACGACCAGCTCATGGGCTTTGAGAGAGACTCTGAAGGAGACTCTCAGGGGGCCAGACC 2157 GAGTGAAGTTGAGGAACCAGGGGTCCAGGGGAGGCCAGGGGTGAGAGGCCAGGGCC Gaps . 0 0; Mismatches 116; Indels Matches 1461; Conservative 2397 2577 2637 2757 1064 2817 1124 1184 2037 464 2277 2337 2457 764 2517 2697 644 704 824 ద ઠે 원 ò g 셤 ò g δ g ઠ 임 g Dp ò 셤 ઠે g ઠે 8 g g d ð qq à 8 ઠે $\dot{\delta}$ 유 à 8 ò 셤 à

1423 3416 creregreacanacerrrregreracerrrrecaacracaceaccaceaccacaa 1543 TGTTTTGAGCACTCGGGGTCCAGCAGCCCTGGGTACTAGTAGCAGGCTCTTCATTC 3476 Human; secreted protein; cytokine; cell proliferation; nutritional supplement; immune modulation; autoimmune disorder; haematopoiesis regulation; tissue growth; haemostasis; inflammation; ss. CTATACCACGGGCCACTGGGACAACTACAAGCGCCACCAGAAGGTGCATGGCCACGGTGG cercaaacercaeardeedeecacacacaedeedaaadeecerreegerdreedeedee TCATCHGATAACCTGAAACGGCACCAGCGCGTCCATACAGGAGAGAAGACCCTACAAGTG CCCCTCTGCCCTTATGCCTGTGGCAATCTGGCCAACCTCAAGCGTCATGGTCGCATCCA CTATACCACAGGCCACTGGGACAACTACAAGCGTCATCAGAAGGTGCATGGCCATGGTGG **CATGAAGACTCACAGTGGTGAGAAACCCTTCCGCTGTGCCCGCTGTCCATACGCCTCTGC** CATGAAGACACACAGTGGTGGAGAAGCCCTTCCGCTGCGCCCGCTGTCCTTATGCCTCTGC CCCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCAACCTCAAGCGTCATGGTCGCATCCA CTCTGGTGACAAACCTTTTCGGTGTAGCCTTTTGCAACTACAGCTGCAACCAGAGTATGAA CCTCAAACGTCATATGCTGCGACACACGGGCGAGAAGCCCTTCCGCTGTGCCACCTGCGC TCATCTGGATAACCTGAAACGGCACCAGGCGTCCACACAGAGAAAAAGCCCTACAAGTG Human secreted protein coding sequence SEQ ID NO: 61. *tag= b note= "potential signal peptide" 186. .224 *tag= e note= "potential signal peptide" 119. .1622 *tag= f note= "potential mature peptide" Location/Qualifiers
177. 1625
/*tag= a
//product= "secreted protein"
180. 218 /*tag= c /note= "potential mature 225. .1622 AGACTCACCTTGAACTA 3493 AGACTCATCCTGAACTA 1800 AAA93131 standard; cDNA; 1996 .218 (first entry) *tag= Homo sapiens 12-JAN-2001 mat_peptide sig_peptide sig_peptide mat_peptide 3477 1784 1664 1724 1304 3057 1364 3117 3177 1484 3237 1544 3297 1604 3357 3417 AAA93131; 1424 2997 RESULT 8 AAA9313 ద 8 8 8 8 ક d G 8 셤 8 B 8 셤 ò 셤 ઠ

Rapiejko

Hall J,

Hoffman H,

Yuan O,

WPI; 2000-549267/50. P-PSDB; AAB23631. Valenzuela D,

(ALPH-) ALPHAGENE INC

19-FEB-1999; 99US-0120680P.
23-AFR-1999; 99US-00296733.
17-AUG-1999; 99US-0155866.
01-CCT-1999; 99US-015747P.
29-NOV-1999; 99US-0167822P.
29-NOV-1999; 99US-0167822P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the coding sequence for a human secreted protein. The sequence was isolated from an adult lung cDNA library. The proteins and coding sequences of the invention can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have tases as nutritional supplements, as cytokine or cell proliferation autoimmune diseases, as haematopoiesis regulators (treating mysloid or autoimmune diseases, as haematopoiesis regulators (treating mysloid or hymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, haemostatic or thrombolytic
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2000US-00552317.
2000US-00598042.
2000US-00598042.
2000US-00620312.
2000US-0063450.
2000US-00653450.
2000US-00653450.
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25-APR-2000;
20-JUN-2000;
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, alzhelmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and SNy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic as and thrombolytic activity, arthritis and inflammation, leukaemias and classes for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
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31.7%; Score 1220.2; DB 4
Best Local Similarity 92.9%; Pred. No. 4.1e-301;
Matches 1272; Conservative 0; Mismatches 97;
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02-MAR-2000; 2000US-018550P.
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Ruben SM Barash SC, Rosen CA,

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 40206; 3071pp + Sequence Listing; English.

AMKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I)

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polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM8169 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                             Query Match
31.1%; Score 1195; DB 4; Length 9266;
Best Local Similarity 81.3%; Pred. No. 2.9e-294;
Matches 1568; Conservative 0; Mismatches 216; Indels 144;
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       Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of a number of human reproductive system related antiqens. These can be use in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding protein of the invention
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preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
31.1%; Score 1195; DB 4; Length 9266;
Best Local Similarity 81.3%; Pred. No. 2.9e-294;
Matches 1568; Conservative 0; Mismatches 216; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9266 BP; 2324 A; 2431 C; 2502 G; 2009 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 7625, 1297pp + Sequence Listing, English
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01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-025186P.
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3078 TGGCCAGGGGCTCCACACAGACTAAGGCACTATAAGGACCAGCCCAACCCATGGG 3137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic Sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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31.1%; Score 1195; DB 4; Length 9266;
Best Local Similarity 81.3%; Pred. No. 2.9e-294;
Matches 1568; Conservative 0; Mismatches 216; Indels 144;
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05-JAN-2001; 2001US-0259678P.
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               ACCTGCGCCTATACCACAGGCCACTGGGACAACTACAAGGGTCATCAGAAGGTGCATGGC 3348
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       CGCATCCACTCTGGTGACAAACCTTTTCGGTGTAGCCTTTGCAACTACAGCTGCAACCAG
                                        CATGOTGGAGGAGGAGCCTGGTCTCTGCCCCTGAGGGCTGGGCCCCACATAGC
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> 23-JAN-2662 (first entry) ABA15877;

5877/c | ABA15877 standard; DNA; 9266 BP

Human, nootropic, neuroprotective, cytostatic, dermatological, virucide, immunosuppressive, antiinflammatory, anti-HIV, antibacterial, vulnerary, antiparkinsonian, antisickling, antiannemic, antiarthritic, cancer, antirheumatic, hepatotropic, cerebroprotective, antiinflammatory; antialiberic, antillacy, antillacy, antillacy, antilorulisant, antifungal, antiparasitic, cardiate, immune disorder, cardiavascular disorder, neurological disease, infection, nephrotropic, gene therapy, vaccine, ds. Human nervous system related polynucleotide SEQ ID NO 8208.

Homo gapiens

WO200159063-A2.

16-AUG-2001.

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01-DEC-2000; 2000US-0256391P.

01-DEC-2000; 2000US-0251160P.

05-DEC-2000; 2000US-0251163P.

05-DEC-2000; 2000US-0251163P.

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08-DEC-2000; 2000US-0251868P.

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08-DEC-2000; 2000US-0251868P.
29-SEP-2000; 2000US-0236369P.
02-OCT-2000; 2000US-0236302P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0239935P.
13-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241785P.
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20-OCT-2000; 2000US-0241786P.
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20-OCT-2000; 2000US-024180P.
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20-OCT-2000; 2000US-0244617P.
08-NOV-2000; 2000US-024647P.
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08-NOV-2000; 2000US-024920P.
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> Š Rosen CA, Barash SC, WPI; 2001-541565/60

(HUMA-) HUMAN GENOME SCI INC.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant)agonists are useful in the nucleic acids, proteins, antibodies and (ant)agonists are useful in the adagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal jand, bone, bone marrow, breast gastrointestinal tract, liver, lung, or urogenital; (b) immune concerns autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid architis and ulcerative colitis; (c) cardiovascular disorders eugh actorial ischaemias; (d) wound healing (e) neurological diseases such as viral, bacterial, fungal and parasitic infections, diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly with the printed in the printed specification that pass obtained in electronic format directly and the printed specification the printed in electronic format directly as the sequence data for sequences Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases. Disclosure, SEQ ID NO 8208; 1701pp + Sequence Listing; English. ###X#XBBBBBBBBBBBBBBBBB

Sequence 9266 BP; 2009 A; 2502 C; 2431 G; 2324 T; 0 U; 0 Other;

2542 7288 2602 7528 2362 7468 2422 7408 2482 2182 7587 2302 2651 2063 GAGACTCTGAAGGAGACTCTCAGGGGGCCAGACCTGGACTTCCCTATGGGCTGAGTGACG
7166 CTATTTCACCAGGAGACTCTCTGGGGGCCAGGCCTGGGCTTGGCTTCCCTATGGGCTGAGCGACG CCCACACAGGGCCTCCCACTCCTGCCCAACCTGTGGCTTTCGATGCTGTGCTCCAC CCCACGCAGGGCCCCCCACCCCCCCCCCCGCCCGACCTGTGGCTTCCGCTGCTGTACTCCAC GGTTACTGTACTCATGCCGGCTGTGCGCTTTCGTGTCCCACTACTCGAGCCACCTGAAGC GGCACATGCAGACACACAGCGGGAGAAGCCGTTCCGCTGTGGCCGCTGCCCATACGCNT CAGCCCAGTTCGTCAACCTGACGCGACATACCCGCACCCATACTGGCGAGAAAGCCCTACC GITGICCCCACTGCCCCTTTGCCTGCAGCCTGGGCAACCTGAGGCGCATCAGCGCA 2003 AAGAGGAAGAGGAAGAAGATGAAGGTGACGGCCACACGACCAGCTCCATGGGCTTTGAGA Greenagaccagagaranahagaccaagaccagacranarranarrangarangagaccah Query Match
31.12; Score 1195; DB 5; Length 9266;
Best Local Similarity 81.33; Pred. No. 2.9e-294;
Matches 1568; Conservative 0; Mismatches 216; Indels 144; GACCAACCCGGCCTCCCAGTCCCACAGAGCAGGGGGACAATGCCCCG---2243 (2363 2543 7227 2183 2303 2423 2483 2603

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6009 ACTGCCCAGCCTCCCACCTGTTTATTTAACTTATTTCAGTGCTTTATAAAAAGGAAACA 5950
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                                                                                                                                                                                                                                                                                                                                                            Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika
Otsuka M, Nagahari K, Masuho Y;
                                                                  2341 CACTACTCGAGCCACCTGAAGCGGCACATGCAGACACACAGCGGGGAGAAGCCGTTCCGG
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                                                   GATTAGGGCCTTGGATTCACCGCCACTGCTCCCAGAGGCTATGGATGAACTGGTTGGGAG
3649 TCAGGGGG-CCATATAGACCAGGGGA-CTTGTCTTAGCTCACGTACCAGATGAGCTAAGT
                                                                                                       -CTGCCCAGCCTTTTAC----TGTTTTAACTTATTTCAGTGCTTTATAAAAGAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel human secretory or membrane proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS2433-ADAS4071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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29.0%; Score 1115.2; DB 7; Length
Best Local Similarity 87.4%; Pred. No. 2.8e-274;
Matches 1305; Conservative 0; Mismatches 144; Indels
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24-JAN-2002; 2002US-0350435P.
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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P-PSDB; ADA55197.
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                                          TAAGACACCAGGGACCAAAGATCTTGGGACATGGGTGGCTGACCTAGGAATGCTTGG

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TAGAAACCACCTTTCTCCCCCGCTGGTCAGGGCT 3600 CCAGAGGCTATGGATGAACTGGTTGGGAG-CTGCCCAGCCT 3777 3481 TCACCTTGAACTAAGTTCTTTTACCTGGGGCTCTAGGAATTAGCCCTATGCCTCT 3540 TCTTC------CC 1167 CACTATATGGACCAGCCTGAATCCCATGGTCAGGGGG-CCA 3659 CACTATAAGGACCAGCCCAACCCCATGGGCGGGGGGCCCA 1283 ITCTTAGCTCACGTACCAGATGAGCTAAGTGATTAGGGCCTT 3718 GCTTGACTGAGGCACTTCATGAGCTCAGTGAGAAGGGCCCT 1343 Ren F, Wang D; Zhang J, Zhao QA; ypeptides, useful for treating disorders such njuries. pressant; cytostatic; gene therapy; cancer; neuropathy; central nervous system; CNS; sease; Huntington's disease; haemostatic; is; Shy-Drager Syndrome; chemotactic; drug screening; arthritis; inflammation; Qian XB, Yang Y, Ma Y, Xue AJ, 78pp; English. , Chen R, I, Xu C, M NO 359. 58 BP. 0.0700104

The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous cystem, such as peripheral nervous injuries, peripheral neuropathy and contains and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Chiteral sclerosis, and Shy-Drager Syddrome. Other uses include the cutilisation of the activity, chemotactic/chemokinetic activity, haemostatic cand thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C. N. & disorders. Note: The sequence data for this patent did not form

Sequence 1558 BP; 331 A; 456 C; 494 G; 277 T; 0 U; 0 Other;

7; 45; Gaps Query Match
21.2%; Score 815.2; DB 4; Length 1558;
Best Local Similarity 85.7%; Pred. No. 1.4e-197;
Matches 1004; Conservative 0; Mismatches 123; Indels 45;

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3691 3751 GCCCCACCTCATAGCCCACCCTCTGTTTTGAGCTCTCGGGGCCCCACCAGCCCTGGGGACT 1203 1407 CTTCACGAGCTCAGTGAGAAGGGCCCTGTATTCACCTCCACTGCCCCCAGGGGCTGTGGA 1467 CABACCGGCTGGGGGGACTGCCCAGCTGCTGTTTAACTTAATTTCAGTGCTTT ---TTTCTCCCCCGCTGGCCAGGGCTCCACAGACTAACGTAGGCACTATAAGGACCA 3634 GCCTGAATCCCATGGTCAGGGG-CCATATAGACCAGGGGA-CTTGTCTTAGCTCACGTA 1347 decemacedearedecededecedearinationecia de december en contra de contra 3574 CCCTTTCTCCCCCCCCCGCTGGTCAGGGCTCCACACAGACTAACCTAGGCCACTATATGGACCA CCAGATGAGCTAAGTGATTAGGGCCTTTGGATTCACCGCCACTGCTGCGAGGGCTATGGA 3752 TGAACTGGTTGGGAG-CTGCCCAGCCTTTTAC----TGTTTTAACTTATTCAGTGCTTT 3514 GCTCTAGGAATTAGCCCTATGCCTCCTGCATTTATACAAATGAACTAGAAACCACCTTT 1204 GCTGGCAGCCGGCTGTCCACAGACTCATCCTGAAC---3692 1290 1242 1144 8 8 8 8 8 8 음 참 셤 ò g à ò

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3847 bp DNA CNRE binding factors and uses thereof. BD234712

RESULT 1 BD24712 LOCUGS DEFINITION ACCESSION VERSION KEYWORDS SOUNCE ORGANISM

ALIGNMENTS

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YUQING B CHEN, MASATSUGU HORIUCHI, VICTOR J DZAU, KOICHI TAMURA CIZNIS/09, A61K31/711, A61K38/00, A61K38/00, A61K95/00, A61P9/00, A61P9/12, A61P9/12, A61P9/12, A61P9/12, A61P9/10, C207K14/47, C12N1/15, C12N1/
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Submitted (10-WAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (bases 1 to 19929)

B iren, B., Linton, L., Nubbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Changalo, M., Campoplano, A., Chang, L., Campoplano, A., Chang, L., Campoplano, A., Chang, L., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farceriar, P., EtzGeradd, M., FitzHugh, W., Gage, D., Gandana, S., Farceriar, P., FitzGeradd, M., FitzHugh, W., Gage, D., Gand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Lindhad, Toh, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindhad, Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Marthews, C., Macdonald, P., Major, J., Nardon, J., Nardon, T., Manchews, C., Macdonald, P., Major, J., Nardon, J., Nardon, P., Marchews, C., Macdonald, P., Major, J., Nardon, J., Nardon, P., Nardon, J., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Ilara, V., Raymond, C., Retta, R., Sanens, R., Sanens, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Severti, M., Subramanian, A., Talamas, J., Tasqe, S., Toplam, K., Travers, M., Travis, N., Trigilio, J., Toplam, K., Travers, M., Travis, N., Trigilio, J., Young, G., Zainoun, J., Zenbek, L., Zimmer, A. and Zody, M., Cannon, M., Street, Submission
AC114619 199296 bp DNA linear HTG 06-JUN-2002
Mus musculus clone RP24-86123, WORKING DRAFT SEQUENCE, 15 ordered
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria: Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (bases I to 1992s6)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-86123
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All repeats were identified using RepeatMasker:
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
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AUTHORS
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COMMENT

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* NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the fizes of the gaps between them are based on estimates that have provided by the submittor.

* The sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* The finished sequence as soon as it is available and the accession number will be preserved.

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* The finished sequence as soon as it is available and the accession number will be preserved.

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                                                         Center project Information
Center project name: 124325
Center clone name: 124325
Center clone name: 86 I 23
Center clone many Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly, program: Phrap; version 0.960731
Consensus quality: 193147 bases at least Q30
Consensus quality: 197247 bases at least Q30
Consensus (ality of agarose-fp
Insert size: 194000; agarose-fp
Quality coverage: 6.1 in Q20 bases; sum-of-contigs
Quality coverage: 6.0 in Q20 bases; sum-of-contigs
                                Contact: sequence_submissions@genome.wi.mit.edu
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Web site: http://www-seg.wi.mit.edu
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/note="assembly_fragment"

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| misc_feature /note="assembly_fragment" misc_feature /note="assembly_fragment" misc_feature /note="assembly_fragment" /note="assemb | 182825 CAGGCAGAGAGAGAAACTGGAGGACCACTGTCCACGGAGGGCTGAAGAC 18 540 ACCGGCAACAGAGAAAAAGAAGGAAACTGGAGGGACTGTCCACGGAGGGCTGAACAC 18 182885 ACCGGCAACAGTGACAAAAAAAGAAGGCCAAGAGGGATTAGTGGTCAACCGGACCTGCCCA 59 600 TGTGGACTGTTTTCTGAGCCCTTGGACCCGAGACTGAGTTTTGTCCTTTTAGCCT 65 182945 TGTGGACTGTTTTCTGAGCCCTTGGACCCGAGACTGAGTTTTGTCCTTTTAGCCT 65 660 TAGCAGTGGTATTCTGAGCCCTTGGACCCGAGACTGAGTTTTGTCCTTTTAGCCT 18 183005 TAGCAGTGGCTATGAGGTGCAGGGGCTGGGGTTTTCTCTCAGCCCATTAGCCT 18 183005 TAGCAGTGGGTATGAGGTGCAGGGGCTGGGTTTCCTTCAGCCCATTAGCCT 18 |

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/organism='Mus musculus
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                           A61K37/48,C12N5/00
CNRE binding factors and uses thereof
Key Location/Qualifiers
source 1..2651
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Pred. No. 0;
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Best Local Similarity 99.7%;
Matches 2643; Conservative
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Rummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2651)

1 (bases) 1 to 2651)

CNRE binding factors and uses thereof

Patent: JP 2002516664-A 16 11-JUN-2002;

THE BRIGHAM AND WOMEN'S HOSPITAL INC

Nus musculus (mouse)

Phy JP 2002516664-A 16

Phy JP 200251664-A 
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AGIP9/00,AGIP9/04,AGIP9/12,AGIP43/00,CO7K14/47,C12N1/15,C12N1/
19,C12N1/21,
C12N5/10,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,C12N15/00, PC
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                                                                                                                                                                                  CCTGCGCCTATACCACAGGCCACTGGGACAACTACAAGCGTCATCAGAAGGTGCATGGCC
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FT source 1. .2289
FT source // Organism='Mus musculus (mouse)'.
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/organism="Mus musculus"
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Baldwin, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F.,
Bryant, M., Budar, C., Burch, P., Burrell, X., Calderon, E.,
Cardenas, V., Chavez, D., Chen, P., Burrell, X., Canderon, S.,
Cardenas, V., Chavez, D., Chen, P., Burrell, X., Chen, Z., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chacko, J., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Dermo, C., Dinh, H., Divya, K.,
Braper, H., Dugan-Rocha, S., Dunn, A., Dinn, R., Dinh, H., Divya, K.,
Fernandez, S., Fihley, M., Flaggo, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garrer, M., Gacra, M.,
Gabisi, A., Ganta, R., Garria, A., Hamilton, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Harvey, Y., Havels, P., Hadhand, W., Handel, S., Hadh, J., Chu, M., Jolivet, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, R., Johnson, R., Johnson, R.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Liu, Y., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorlesuhewa, L., Loudon, P., Lozado, R., J., Lu, X., Ma, J.,
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274060 bp DNA linear #FG 13-NOV-2002 autories of the CH230-9D7, WORKING DRAFT SEQUENCE, 3 unordered pieces.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Worley, K.C.

Direct Submission

AL Contest (16-28P2-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

CE 3 (bases 1 to 274060)

RS Rat Genome Sequencing Consortium.

Direct Submission

AL 
* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a "working draft" sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Phrap; version 0.990329
Consensus quality: 251078 bases at least Q40
Consensus quality: 255677 bases at least Q30
Consensus quality: 258294 bases at least Q20
Estimated insert size: 259919; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Contact: project Information
Center project Information
Center clone name: CH330-9D7
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Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                  Query Match

54.4%; Score 2092; DB 2; Length 274060;

Best Local Similarity 73:5%; Pred. No. 0;

Matches 3373; Conservative 0; Mismatches 315; Indels 902;
                                                                             1 270488: contig of 270488 bp in length
489 270588: gap of unknown length
589 271093: gap of unknown length
272033: gap of unknown length
584 274060: contig of 1967 bp in length
584 274060: contig of 1967 bp in length
584 274060

Accion/Qualifiers
1. 27466

Accion/Qualifiers
1. 27466

Accion/Capalism="Rattus norvegicus"

Adb Aref="Genomic DNA"

Alb Aref="Genomic DNA"
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| Oy 2217 AGCCTGTCAGCTGTGTGGGGGCCCACAGGTGAGGGCCGTGTT | Db 262333 AGCCTGTCAGCTGTGTGGGGGGGCCGACAGGTGAGGGGCCGTGTT Ov 2277 GGGTGGGGGGCCCCCCCCCCCCCCACGGTGGTGTGT | 262273 GGGTGGGNNNNNN | D | 2389 | 262153 | Qy 2449 CATACCCGCACCATACTGGCGAGAAGCCCTACCGTTGTCCCC | 262093 | 2509 | 26 | 2569 | Db 261973 TGCCCAACCTGTGGTTTCCGATGCTGTGCTCCACGACCAACCC | Qy 2629 GAGCAGGAGGACAATGCCCCGGACGATCAGA | 261913 | Qy 2661 | 26 | Qy 2662 AAIGCGCTGAICCTGCCAGACTIGAGICTICAIGIGCCACCAG | 261793 | 2722 | 261733 | 2782 | 56 | by 2842 gaggecageragerageaagereceargreragegegegeracarge | Db 261613 GAGGGCAGCTTGGGAACTGCCATGTGTGGGCCTGCATGC | QY 2902 GTTGCCACTGGGGGGCCCCTGGTGACAAAGGCTTTG | Db 261553 GGTGGCAGGGCCCCAGGGCCCTAGTGACAAAGGCTTTG | Qy 2962 TTTGCCACTCACTACCCCAACCACCTCGGCTCGGGACATGAAGA | Db 261493 TTTGCTACTACTACCCCAACCACTGGCCCGGCACATGAAGA | Qy 3022 CCCTTCCGCTGTGCCCGCTGTCCATACGCCTCTGCTCATCTCG | 26 | 3082 | 261373 | | Db 261313 AACCTGGCCAACCTCAAGCGTCACGGTGTATCCACTCTGGTV |
|--|--|--|---|---|-----------|--|-----------|---|-----------|---|---|--|-----------|---|-----------|---|-----------|--|-----------|--|-----------|--|---|---|--|---|---|---|------|---|---|---|--|
| 263473 GTGCAGTTCACAACAGCTGGCTCCCTGGTTCGAATTATGGGAACGGGTTGTGAGGGAGAT 263414 | 1894 TCCACAAGCACCCTCCTTTAGTGGATACTGAAGATTCCTTCGACGAAGGTCCTGGG 1953 263413 TCCACAAGCACCTCCCTCTTTAGTGGATACTGAAGATTCCTTCGACGAAGGACTGGG 263354 | 1954 GCCTGGTGTTGGAGGGAITTGCTACTAGGCCAAGATCTGGAGTTTGAAGAGGAAGG 2013 | 2014 GAAGAGGATGAAGGCGGCCACAACGACCAGCTCATGGGCTTTGAGAGACTCTGA- 2072 | 263293 GAAGAGGAAGGTGACGGCCACAACGACCAGCTCATGGGCTTTGAGAGACTCTGAA 263234 | 2073 2072 | 263233 GGTGTGTTTAAGGGTCGTGGTTAAGGATAAGAGGCTTTTGGTAACTCAAGCCCTTTAGAA 263174 | 2073 2072 | 263173 GGCGGTGTTAGCGACCAAAACACCACTTCTTTTACAACCTAGCAGCAGCATTTTGGTGA 263114 | 2073 2072 | 263113 GITGAAGTICTGGGTCCGGGCTAAAGGTGGTGTGAATACAAGGGTGGGGTAGCCACATTTC 263054 | 2073 2072 | 263053 TTATGTACCCCTCAAGAGGTTCATGGAAGGGAATTATGTAAATAAGCTACTCTTAAAACT 262994 | 2073 2072 | 262993 CTCTGGCTAGTAGCAGTAGATTCTTTTTTTTTTCAGGTTTCAGTTTTCTGCCCTTAAGTCT 262934 | 2073 2072 | 262933 CICCTCGITTATTICTTGGGTAITTTTTAAAGTCAGAGAAACCATATAAAAGAATCTGC 262874 | 2073 2072 | 262873 CCTTTCTGTGTAATTTGCACTACATTGCTCCCACTTTCTCCAAATTGTGCCTACTTGAGA 262814 | 2073 2072 | 262813 TGGCTTTCATTTCATAATCAGCCTTATAAAAAGGAGCCTTACTAAACCAGGGTTTACA 262754 | 2073 2072 | 262753 AAAAAGAICITGGGGTCTTIAIATTITIACTTATCTCATAITGTTGCTTCACATCAGCCT 262694 | 2073 2072 | 262693 GTACTCCACTTCAAGCCTGTGATATTTCCATTTGTTGGAAATGATAAGTCACCCCTAGT 262634 | 2073 2072 | 262633 GTTAGTAATTAGGCTCAAATAGAATGAAATCAAAGGTGAGGCAGAATAAGTGGGGGCTTTT 262574 | 2073 2072 | 262573 TGTGAGAAATGAGAATTTGGAACTCAGTCTTGAGCCATGTTGATTGGTTTCTTTTTT 262514 | 2073 | 262513 TTTTCTTTTTTCCTCCTTCCTTTCTGTTTCACCAGGAGACTCTCAGGGAGCCAGACC 262454 | 2097 IGGACTTCCCTAIGGGCIGAGIGACGACTGGGGGGGGGGG | | |
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TGACAAACCTTTCGGTGT 3201 ||||||||||||||||| TGACAACCTTTTCGGTGT 261254 AGGIGGIGCCAGITICCIG 2721 GCGAGGAGAGGCTGGAGGG 2901 GGATAACCTGAAACGGCAC 3081 ||||||||||||||| |GGATAACCTGAAACGCCAC 261374 AGGGCTCCCACTCCTCC 2568 CCGCCTCCCAGTCCCACA 2628 ATATCTCATTGTTCCCACA 261794 STICGICAACCIGACGCGA 2448 CACTGCCCTTTGCCTGC 2508 3AGCACCAGAGATCTTGGG 261854 NNNNNNNNNNNNNTGC 262214 GGAGACACGGGGAG 2388 SACTCACAGTGGTGAGAA 3021 .----- 2660 ----- A 2661 TACTCATGCCGGCTGTGC 2328 TTGTGGGGCAGGAGGGCG 2276

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ATTGGTTGGCTAGCAGCGCATCACAATCACTTCCTGGTCATGCTGCTGCGACTGCGCTCCGGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TGTACAGCCCATGAACTACGCATCCCGTGTTGCTCTGCGGTGGCGGAAGCGGAAGCGGGT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels 316; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.7%; Score 1988.4; DB 6; Length 2336; Best Local Similarity 87.8%; Pred. No. 0; Matches 2328; Conservative 0; Mismatches 7; Indels 316;
A61K37/48,C12N5/00
CNRE binding factors and uses thereof
Key Location/Qualifiers
source 1. .2336
/organism='Mus musculus (mouse)'.
Location/Qualifiers
                                                                                                                                                                                                                                       1. .2336
/organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
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3202 AGCCTTTGGAACTACAGCTGCAACCAGAGTATGAACCTCAAACGTCATATGCTGCGACAC 3261
261253 AGCCTTTGCAACTACAGCTGCAACCAGAGCATGAACCTCAAACGTCATATGCTGCGACAC 261194
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PN 19-20251664-A/15
PN 17-20251664-A/15
PP 23-ARR-1999 UP 2000545541
PR 24-APR-1999 US 60/082997
PY 19-20210 CHEN, WASATSUGU HORIUCHI, VICTOR J DZAU, KOICHI TAMURA PC CIZNIS/09, A6IR31/711, A6IR38/00, A6IR48/00,
PC A6IR48/00,
PC A6IR48/00,
PC A6IR48/00,
PC A6IR48/10, A6IP9/04, A6IP9/12, A6IP43/00, CO7K14/47, CIZNI/15, CIZNI/PC CIZNIS/10, CIZNI/15, CIZNI/15, CIZNI/15, CIZNI/15, CIZNI/15, CIZNI/16, CIZNI/16, CIZNI/16, CIZNI/16, CIZNI/16, CIZNI/10, CIXNI/10, CIZNI/10, CIXNI/10, CIZNI/10, CIZNI/10, CIZNI/10, CIZNI/10, CIZNI/10, CIZNI/10, CIZNI/10, CIZNI/10, CIXNI/10, CI
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Chen, Y. E., Horiuchi, M., Dzau, V. J. and Tamura, K.
CNEE binding factors and uses thereof
Patent: JP 202516664-A 15 11-JUN-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL INC
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| 1506 CCCCCTCTGTGACANCCTTTTCGTGTGACCTTTCGACCTACCTCACCACCACCACCACCACCACCACCACCACCA | RESULT 7 BC058976 LOCUS LOCUS LOCUS MAS musculus RIKEN CDNA D430028M17 gene, mRNA (CDNA Clone MGC:67303 ACCESSION ROCS8976. I G1:37589246 VERSION RC58976. I G1:37589246 MS musculus (house mouse) NGANISM MS musculus (house mouse) RC58976. I G1:37589246 MS musculus (house mouse) RC58976. I G1:37589246 AUTHORS KLUP Feingland (Craniata) Vertebrata; Euteleostomi; Butharyota; Modata; Craniata; Vertebrata; Euteleostomi; REFERENCE ORGANISM REFERENCE Strausberg KL., Feingland (E.A., Grouse, L.H., Derge, J.G., Altschul, S.F., Zeeberg, B., Wagner, L., Schemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheefer, C.F., Bhat, M.K., Diatchenko, L., Marusina, R., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., |
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2817 CTGTGGACAGGAACTGGAGGAGGTGAGGGCAGCAGGCTGGGAGCTGCCATGTGTGGGGCG 2876
JSMNLKRHMLRHTGEKPFRCATCAYTTGHWDNYKRHQKVHGHGGAGGPGLSAPEGWAP
                                                                                                            COGS048, FOG: Zn-finger [General
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1432. .1653
/note="COG5048; Region: COG504
function prediction only]"
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.

Location/Qualifiers

1. .220
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Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A. Schein, J.B., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
E. 22388257

E. 22388257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (01-0CT-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: agapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
PC Cancer Agency, Vancouver, BC, Canada
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379. .1818
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Strausberg, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
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MEDLINE
PUBMED
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COMMENT
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725

785

1085 2816 1145

2756

2516

2576

905

2636

2696

| | NON DS | SOURCE HOMO ORGANISM HOMO Eukary Mamma | REFERENCE I SOGA AUTHORS I SOGA Yamam | TITLE JOURNAL | FEATURES source | ORIGIN | Query Match Best Local Simi | Matches 1727; Qy 1885 GAG | Db 102 GAG | Oy 1945 GGT | Db 162 dGA Qy 2005 GAG | Db 222 GAG | Oy 2065 GAC | Db 282 GAC | Qy 2125 GAG | Db 342 GAG | 2185 | DD 402 CCA | 462 | Cy 2305 TTA | Db 522 CTA | Qy 2365 CAC | Db 582 CAC | Qy 2425 GCC | Db 642 GCC | Oy 2485 TGT | Db 702 TGT |
|----|--|--|--|---|---|---|---|--|--|---|---|--|---|--|---|--|--|---|---|-------------|---|---|--|-------------|-------------------------|---------------------|------------|
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| QQ | & g | 8 8 | 8 8 | રું કે - | & 43 | ò | d G | & A | δ̈ | q | & A | ð | d d | δ | ପ୍ଧ | ð | q a | රි සි | δ | a a | δŏ | q | à | đ | à | ପ୍ଧ | |

RESULT 8

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485 TGTCCCCACTGCCCTTTGCCTGCAGCAGCCTGGGCAACCTGAGGCGCGCATCAGCGCACC 2544
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amoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
chika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
tho,Y.
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PAT 15-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTGGGGGCGGCGCGCGCACTAAGTGCGGAGAGTGAAGTTGAGGAACCAGGCCAGGGGT 2184
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alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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nilarity 88.6%; Fred. No. 0;
Conservative 0; Mismatches 178; Indels 44; Gaps
linear
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      DNA
2013 bp D1
ence 1582 from Patent EP1347046.

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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                                                                                                                                                                     4458.1 GI:39920593
                                                                                                                                                                                                                                                                                   sapiens (human)
                                                                                                                                                                                                                                                                                                                                                      sapiens
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| | AKO96933 AKO96933 2013 bp LOCUS LOCUS ACCESSION Homo sapiens CDNA FLJ39614 fis, to ZINC FINGER PROTEIN 83. ACCESSION AKO96933 AKO96933 VERSWORDS OLIGO capping; fis (full insert SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM EUKARYOCA AMERAZOA; Chordata; Cr Mammalia; Eutheria; Primates; Ca Mammalia; Eutheria; Primates; Ca AUTHORS KOdaira, H., Furuya, T., Takahashi | Kaminatark., Katsuca, Kawai-Hicking Sugiyama, T., Irie, R., Oteuki, T., Yamamoto, J., Isono, Y., Kawai-Hickinura, K., Yamashita, M., Marakani, Kimura, K., Yamashita, M., Maneboo, Kikuchi, H., Murakawa, K., Kaneboo, Magahari, K., Masuho, Y., Nagai, K., Nagai, K., Masuho, Y., Nagai, K., Nagai, K., Masuho, Y., Nagai, K., Nabai, K., Masuho, Y., Nagai, K., Masuho, Y., Nagai, K., Masuho, Y., Nagai, K., Masuho, Y., Masuho, Y., Masuho, Y., Masuho, Y., Masuho, M., Ma | Research Association for Biotect construction: Helix Research Int Key Technology Center etc.); 5'- HRI, and Biotechnology Center, 1 Evaluation; clons selection for FAB; annotation: HRI and RAB. Location/Qualifiers 1. 2013 Organism='Homo sapien: Mol_type="mRNA" Abstraction Abstraction Abstraction Abstraction Abstraction Abstraction Abstraction Abstraction Abstracti | /clone_Tib="SMINT2" /note="Cloning vector: 2671706 /note="unnamed protein /codon start=1 /protein_id="BAC04903. /db_xref="G1:21756543" /translation="MGFREDSE GROGARGRREPACQLCGGPTG IKRHMQTHSGERCPRCGGRCPYA RHQRTHAGPPTPPCFTCGFRCC GGASFLPDCGQLRGEGELGGT |
|--|---|--|--|--|
| 8 6 8 6 8 8 | R S S S S S S S S S S S S S S S S S S S | . RB | | |
| 2545 CACACAGGGCCTCCACTCCTGCCCAACCTGTGGCTTTCGATGCTGCTGCTGCA 2604 762 CACGCAGGGCCCCCCACTCCTGCCGACCTGTGGCTTCTGTGTTGTTGTTCTCACGA 821 2605 CCAACCCGGCCTCCCACACACACAGAGCAGGGGACAATGCCCGGACGATCCAGAAAAT 2664 822 CCAGCCGGCCTCCCAGTCCCACACAGAGCAGGGGCGTGCCCGGACGATCCGAAAAT 2664 824 CCAGCCGGCCTCCCAGACTTGAGCTCTCATGTGCCCCGGCGGCCCGGCGACCTGAAAAT 881 825 CCAGCCCGGCCTCCCAGACTTGAGCCTCCATGTGCCCAGTTTCCTGCCA 7224 826 GCCTCATCCTCCAGATTTGAGCCTCCATGTGCCACAGTGCTCCCAGTTTCCTGCCA 7224 827 CACTGTGGCAACTTGCAGATTTGAGCCTCCATGTGCTGCCAGTTTCCTGCCA 7224 827 CACTGTGGCAACTTGCAGATTTGAGCCTCCATGTGCTGCAGTTTCCTGCCA 7224 828 GCTTGTGGCAACTTGCAGATTTGAGCCTCCATGTGCTGCAGTTTCCTGCCA 7224 829 CATGTGGGCAACTTGCAGAGGGGAGGCCTCTGCGGAACTGCAACACACTG 7001 | | | | 3445 CTGGGGGCACTGGGGGGCGGGCTGTCCACACACACACACA |
| 8 6 8 6 8 6 8 | 1 8 8 8 8 8 8 8 | 8 6 8 6 8 6 8 8 | 8 6 8 6 8 6 | 6 8 6 8 6 8 6 |

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ao Isogai, FLJ Project (HRI Team); 2-6-7
Chiba 292-0812, Japan
Tel:81-438-52-3975, Fax:81-438-52-3986)
project supported by Ministry of
of Japan; CDNA full insert sequencing:
otechnology (RAB); CDNA library
h Institute (HRI) (supported by Japan
i S'- & 3'-end one pass sequencing: RAB,
er, National Institute of Technology and
for full insert sequencing: HRI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anda, K., Kondo, H., Yokoi, T.,
tashi, M., Kikkawa, E., Omura, Y., Abe, K.,
o, K., Tanikawa, M., Yamazaki, M.,
r., Sato, H., Wakamatau, A., Ishi, S.,
-Hio, Y., Saito, K., Nishikawa, T.,
suo, K., Nakamura, Y., Sekine, M.,
tehori, K., Takahashi-Fujii, A.,
tehori, K., Takahashi-Fujii, A.,
ti, K., and Isogai, T., Sugano, S.,
ti, K. and Isogai, T.
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TGEGPCCGAGGPGGPLLPRLLYSCRLCTFYSHYSSH
YASAQUWUTKHTRHTGERPYRCPHCPFACSLIGNLR
CCTPRPARPARPPSPTEGGGAVERRPEDALLLPDLSLHVPP
GTGSEPLPELLFPWTCRGCGGELEEGEGSRLGAAMCGR
                                                                                                       1924
                                                                                                                                               CCAGCCTTTTAC----TGTTTTAACTTATTT 3797
                                                                                                                                                                            mRNA linear PRI 15-JUL-2002 clone SMINT2000176, weakly similar
GGGCCTTGGATTCACCGCCACTGCTCCCAGA 3742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata, Vertebrata, Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                       : pME18SFL3"
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| 7 290 1 296 1 1 1 8 | OY 2965 GCCACTCACTCACCCCAACCCCTGGCTCGCACATGAAGACTCACAGTGGTGAGAAACCC 3024 | 124 | Db 1302 CGCGTCCATACAGAGABAGCCCTACAAGTGCCCCTCTGGCCTTATGCCTGTGGCAAT 1361 Qy 3145 CTGGCCAACCTCAAGCGTCATGGTGGTGGTGACAAACCTTTGGTGTGTAGC 3204 Db 1362 CTGGCCAACCTCAAGCGTCATGGTCGATCCACTCTGGTGACAAACCTTTTGGTGTGAGC 1421 | 3205 | GCGAGAGAGCCCTTCCGCTGTGCCACCTGCGCCTATACCACGGGCCACTGGGACAACTAC 154 AAGCGTCATCAGAAAGGTGCATGGCCATGGGAGAAGAGGGCCTGTGTCTCTGCCCT 338 | 1542 3385 | 1602 | 1662 | 1709 | 1749 GCCACCTTTTTCTCCCCGGTGGCCAGGGGTCCACACAGAGCTAACGTAGGCACACAAAAAAAA | 1805 | 1865 | | 1985 CAGTGCTTATAAAAGGAAACACTAAC | RESULT 10 BCG52282 LOCUS BCG52282 2159 bp mRNA linear PRI 08-OCT-2003 |
|--|--|------|--|--|---|---|---|--|---|--|--|---|--|---|---|
| CMRGEAGGGASGGPQGESDKGFACSLCPFATHYPNHLARHWKTHSCEKPFRCARCPYA SAHLDNLKRHQRVHTGEKPFKCPLCPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCN QSMNLKRHMLRHTGEKPFRCATCAYTTGHWDNYKRHQKVYGHGGAGGPGLSASEGWAP PHSPPSYLSSRGPPALGTAGSRAVHTDSS" Query Match Query Match Best Local Similarity 88.6%; Pred, No. 0; Matches 177. Conservative 0. Mismatches 178. Indels 44. Gads 6: | CONSELVACIVE GGGGGGATTCCACAAGCACCCTCCCTCTTAGTGGATACTGAAGATTCCTTCGACGAA 19 | 1945 | OY 2005 GAGGAAGGGGAAGGAGGAAGGTGACGCCACAACGACCACTATGGCCIIIGAGAAA 2004 DD 222 GAGGAAGAAGAAGAAGAAGAGAAGGCAACGGCAACGACGA | Db 282 GACTCGGAAGGACACTCTGGGGGCCTGGCCTGCCTATGGGCTGAGCGACGAT 341 Qy 2125 GAGTCTGGGGGCGGCCACTAAGTGCGGAAGATTGAAGAACCAGGGGT 2184 | Oy 2185 CCAGGGGAGGCCAGGGCAGGCCAGCCCAGCCTGTCAGCTGTGTGGGGGCCGACA 2244 | Qy 2245 GGTGAGGGCCGTGTTGTGGGGCCACAGGGGGGGGGGGCCCCCCCC | Qy 2305 TPACTGTACTCATGCCGGCTGTGCGCTTTCGTGTCCCACTACTCGAGCCACCTGAAGCGG 2364 | Oy 2365 CACATGCAGACACACGGGGAGAAGCCGTTCCGCTGTGGCCGCTGCCCATACGCNTCA 2424 | Qy 2425 GCCCAGTTCGTCAACCTGACGACATACCCGCACCCATACTGGCGAGAAGCCCTACCGT 2484 L | Oy 2485 IGTCCCCACTGCCCCTTTGCCTGCAGCAGCAGCAACCTGAGGCGGCATCAGCGCACC 2544 | Oy 2545 CACACAGGGCTCCCACTCCTGCCCAACCTGTGGCTTTCGATGCTGTGCTGCGG 2604 | Oy 2605 CCRACCOGGCCTCCCACAGAGCAGGACAATGCCCCGACGACGATCAGAAAAT 2664 | Oy 2665 GCGCTGATCCTGCCAGACTTGAGTCTTCATGTGCCACAGGTGGTGCCAGTTTCCTGCCA 2724 | Oy 2725 GACTGTGGGGGGGGGGGGGGGGGGGGGTTGTGTGGGACTGGATCCGAACCACTG 2784 | Qy 2785 CCAGAGCTACTGTTCCCTTGGACCTGCGGGGCTGTGGACAGGAACTGGAGGAGGGTGAG 2844 |

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Best Local Similarity
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Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/Drp
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Contact: nisc mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Broks,S.,
Dietrich,N.L., Granite,S., (Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Malker,M.A., Wetherby,K.D., Wiggins,L.,
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                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

12. (basea 1 to 2159)

13. Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Rlausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haich, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Staplecon, M., Soares, W.M. B., Bonaldo, M.F., Casarant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

McKernan, K.J., Mullahy, S.J., Boask, S.A., McEwant, F.L.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Wuzny, D.M., Sodergren, B.J., Lu, X., Glbbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Garen, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNs, squences

11. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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1. .2159
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Submitted (02-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
o sapiens hypothetical protein FLJ32203, mRNA (cDNA clone:59968 IMAGE:5467936), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 2159)
                                                                                                                                 Homo sapiens (human)
Homo sapiens
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                                                                                                                                                             ORGANISM
        DEFINITION
                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
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MEDLINE
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AUTHORS
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| Qy 3657 -CCATATAGACCAGGGA-CTTGTCTTAGCTCAGGTGACCTAGTTGATTAGGG 3714 Db 1957 CCCATATAGGACTTGACTTGAGGACTTCATGAGTTCAGTGAGAGGG 2016 Qy 3715 CCTTGGATTCACCGCCACTGCTCCCAGAGGCACTTGATGATGATGAGGAGG-CTGCCCA 3773 Db 2017 CCCTGTATTCACTTGCTCACTGCTCGAGGGCTGGGAGACTGCCCA 2076 Qy 3774 GCCTTTACTGTTTTAACTTATTCAGTGCTTTATAATAAAGGAACTTAACAGA 3829 Db 2077 GCCTCCACTGTTATTTAACTTATTTCAGTGCTTTATAATAAAGGAAACACTAACAAA 2136 Qy 3830 AAMAAAAAAAAAAAAA 3847 Db 2137 GCCAAAAAAAAAAAAA 2154 | RESULT 11 AX274856 LOCUS LOCUS LOCUS DEFINITION Sequence 121 from Patent W00172777. ACCESSION AX274856 VERSION AX274856,1 GI:16547488 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) Mammalia, Eutheria, Primates, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. | REFERENCE 1 AUTHORS Hillman, J.L., Baughn, M.R., Yue, H., Lal, P., Lu, D.A., Patterson, C., Azimzai, Y., Bandman, O., Tang, Y.T., Mathur, P., Shah, P., Au-Young, J. and Reddy, M. Tanscription factors JOURNAL Patent: WO 0172777-A 121 04-OCT-2001; Incyte Genomics, Inc. (US) Incyte Genomics, Inc. (US) FEATURES I. 1975 //organism="Homo sapiens" //db refe="Homo sapiens" | ORIGIN Query Match Query Match Query Match Best Local Similarity 88.6%; Pred. No. 0; Matches 1707; Conservative 0; Mismatches 176; Indels 44; Gaps 6; Qy 1917 AGTGGATACTGAAGATTCTTCGACGAAGGTCCTGGGGCCTGGTGTTGGAGAGGATTT 1976 Db AGTGGATACTGAAGATTCCTTCGACGAAGGACCGGGGCCTTGGTATTGAAGATTT 145 Oy 1977 GCTACTAGGCCAAGATTTGAAGAGAAGAAGAAGAAGAAGATGAATTT 145 | 146 |
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| 854 GGGCAACCTGAGGCATCAGGGTACCCAGGCGCCCCCCACTCCTCCCTGCCCGAC 913 | 2817 CTGTGGACAGGAACTGGAGGGGTGAGGCAGGAGGCTGGGAGCTGCCATGTGGGGCG 2876 1154 CTGTGGACAAGAGCTGGAGGGTGAGGGTAGTGGGCTGGGAGCTGCCATGTGTGGGCC 2876 1154 CTGCATGCGAGGAGGCTGCAGGGGTTGCCACTGGGGACCCCAGGGCCCTGGTGACAA 2936 1214 CTGCATGCGAGGAGGCTGGAGGGTTGCCACTGGGGAGCCCCAGGGCCCTGGTGACAA 1273 2937 AGGCTTTGCCTGTAGTTTATCCCCTTTGCCACTGCCCAACCCCAGGCCCCGGGCCCGGGC 2996 1274 AGGCTTTGCCTGTAGTTTATCCCCTTTGCCACTATCCCAACCACTGGCTCGGCT 2936 1274 AGGCTTTGCCTGTAGTTTATCCCCTTTGCCACTATCCCAACCACTGGCTCGGCT 1333 | 2997 CATGAAGACTCACAGTGGTGAAACCCTTCCGCTGTGCCGCTGTCCATACGCCTCTGC 3056 | 17.7 CTCTGGTGACCAACCTTTTCGGTGTAGCCTTTGCAACTACAGCTGCAACCAGGGTATGAA 3236 1514 CTCTGGTGACAAACCTTTTCGGTGACCTTTGCAACTACAGCTGCAACCAGGCATGAA 1573 1514 CTCTGAAACGTCATTGCTGCGACACAGGCGTTTCGCTTGTGTGCTGCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG | 3357 AGCAGAGAGGCCTCGTCTCTGCCCTGAGGCTGGGCCCCACCTCATAGCCCACCTC 1694 GGCAGGAGGCCTCGCTCTGCCTTGAGGCTGGGCCCCACCTCATAGCCCACCTCT 1753 3417 TGTTTTGAGCACTCCGGGGTCCAGGCTCTGGGAGCCTCTCATTC 3476 1754 TGTTTTGAGCTCTCGGGGTCCAGGGCTGGGGCTGTGGCAGCCTTTCATTC 3476 1754 TGTTTTGAGCTCTCGGGGTCCAGCGCTGGGGCTGTGGCAGCCGTTTCATTC 3476 1754 TGTTTTGAGCTCTCGGGGTCCAGCGGCTGGGGCTGTGCCACCC 1813 3477 AGACTCACCTGAACTAACTAAGTCTTTTACCTGGGGCTCTAGGAATTAGCCCTATGCC 3536 1814 AGACTCATCTGAACTAACTAAGAACCACCTTTCCCTTTCTCCCCGGTGGTCAGG 3596 1841 CCCCATGTTTTATACAAATGAAACCAAGAACCACTTTCCCCCGCTGGTCAGG 3596 1841 CCCCATGTTTTATACAAATGAAACCAAGACCACTTTCTCCCCCGCTGGTCAGG 3596 1841 CCCCATGTTTTATACAAATGAAACCAAGACCACCTTTCTCCCCGCTGGTCAGG 3596 1841 CCCCATGTTTTATACAAATGAAAGCCACTTTCTTCCCCCGCTGGTCAGG 3596 1841 CCCCATGTTTTATACAAATGAAAGCCACTTTCTTCCCCCGCTGGTCAGG 3596 1897 GGTTCCACAAGACTAAAAGGCACTATATAGGAACCAGCCTGAACCCATGGGCGGGG 3656 1897 GGCTCCACAAGACTAAAAGGCACTAATAAGGACCAAACCCCATGGGCGGGGGG 3656 1897 GGCTCCACAAAAACTAAAAGGCACTAATAAGGACCAAACCCCATGGGCGGGGGG 3656 1897 GGCTCCACAAAAACTAAAAGGCACTAATAAGGACCAAACCCCATGGGCGAGGGGG 1956 |

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 195880)

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                                                                                                                                                               Similarity 86.2%; Score 1367.6; DB 6; Length 1996; Similarity 86.2%; Pred. No. 0; Observative 0; Mismatches 210; Indels 45;
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                       Query Match
Best Local Simi
Matches 1598;
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COMMENT

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505. .2520
note="similar to Homo sapiens BST AW327943 (NID:g6798438)
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hote="similar to Homo sapiens EST AW327944 (NID:g6798439)
                                                                                                                                                        A transpson exists in the growth of this clone which has been deleted from the finished sequence. This transposon would insert after base 78210. Unsure bases exists between bases 165498 to 16550s. Un unresolved tradem repeat exists between bases 4000 to 6435. Polymorphisms have been identified between AC009427 and AC074117. Data from AC009427 was used to finish this clone,
                                                                  NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-413M20;
actual end is at base position 195880 of RP11-413M20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4780. .6423
//noce="cpd_island (%GC=74.2, o/e=0.70, #CpGs=131)"
/spt_family="SVA"
5926. .5950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11537 .3202
/note="similar to Homo sapiens EST AU130518
and coworkers at http://www.chori.org
VECTOR: pBACe3.6
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3651_3671
/rpt_family="(TTTTA)n"
3953_3995
/rpt_family="MER1_type"
3962_3990
                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
|mol_type="genomic DNA"
|db_xref="taxon:9606"
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4285. .4331
/rpt_family="MER1_type"
4515. .4593
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'rpt_family="MER1_type"
1646. .3952
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/rpt_family="AT_rich"
2959. .3251
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt family="AT_rich" 996. .4284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="RP11-413M20"
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/rpt_family="Alu"
1518. .1538
/rpt_family="(A)n"
1546. .1866
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/rpt_family="Alu"
501. .647
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/rpt_family="Alu"
221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="L1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="L1"
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map="2"
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Mapping information for this clone was provided by Dr. John D.
Mapping information of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (08-FBB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
7 (Dases 1 to 195880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                        Submitted (14-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (05-FEB-2002) Genome Sequencing Center, Washington
Nulversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63109, USA
6 (bases 1 to 195880)
                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (01-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 53108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this close. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence was finished as follows unless otherwise noted:
                                                                                               2 (bases 1 to 195880)
Sun, H., Kozlowicz, A. and Dignan, G.
The sequence of Homo sapiens BAC clone RP11-413M20
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       foward a complete human genome sequence
denome Res. 8 (11), 1097-1108 (1998)
         Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                           3 (bases 1 to 195880)
Waterston, R.H.
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Waterston, R.H.
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Waterston, R.H.
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                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
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| /rpt_family="GC_rich" repeat_region 59686968. | \triangle \trian | 2363 GGCACATGCAGACACACAGGGGGGAGAAGCCGTTCCGGTGTGGGCGGTGCCCATACGCNT 2422 |
|--|--|---|
| repeat_region 62936345 /rpt_family="GC_rich" repeat_region 69426971 | ે દે | 2423 |
| /rpt_ramily="(A)n" repeat_region 7085. 72085. 7208 /rpt_family="L2" | 8 8 | GTTGTCCCCACTGCCCCTTTGCCTGCAGCAGCCTGGGGGGCAACCTGAGGGGGGGG |
| | අු | |
| repeat_region 76467800 /rpt_family="MER1_type" repeat_region 90579347. | & & | 2543 CCCACACAGGCCTCCCACTCCTGCCCAACCTGTGGCTTTTCGATGCTGTGCTCCAC 2602 |
| repeat_region 995_ramin_f_rit /rpt_family="L2" repeat_region 10029_ 10071 | ł & | GACCAACCCGGCCTCCCAGGCAGGAGGGGGACAATGCCCCGACGATCAGA |
| | අ ද | 167542 GACCAGCCCGGCCTCCCAGTCCCACAGAGGGGGGGGGGG |
| /_ppramily="logion" | g q | GTAAGACACCCAGGGACCAAAGATCTTGGGACATGGGTGGCTGACCCTAGGAATGCTTG |
| .10886 mily="L1" .11178 mily="L1" | λό d | 2661 |
| repeat_region 1179. 11483 /rpt_family="L1" repeat_region 11461. 11491 | ે દ | |
| repeat_region 11464. 11603 /rpt_family="Alu" repeat_region 11603. 12618 | 8 8 | AGGGAGAGCTTGTGTGGAACTGGATCCGAACCACTGCCAGAGCTACTGTTCCCTTGGAC |
| <u> </u> | g & | 167782 AGGGGGGCCTCTGCGGGACTGGATCAGAACCACTGCCAGAGCTGATTCCCTTTGGAAC 10701. 2808 CTGCCGGGGGCTGTGGAACTGGAAGAGGGTGAGGGCAGCAGGCTGGGGAGCTGGCGAT 2867 |
| repeat_region 12673. 13130 /rpt family="ERVL" | qq | CTGCCGGGGCTGTGGAGGAGGAGGAGGGTGAGGGTAGTCGGCTGGGAGGCTGCAT |
| repeat_region 1314515421 /rpt_family="L1" repeat_region 1323713292 /rpt_family="L1" | જ વ <u>ે</u> | 2868 GIGTGGGCCTGCAIGCGAGGAGAGCTGGAGGGGTTGCCACTGGGGGACCCCAGGGCCC 2927 167902 GIGTGGGCGCTGCAIGCGAGGAGAGGCTGCAGGGCCCAGGGGCCCCAGGGCCC 167961 |
| .13408 .2.6%; Score 1255.2; .2.2%; Pred. No. 3.7e- | λ δ | 2928 IGGIGACAAAGGCTTIGCCIGIAGTITAIGCCCCTTIGCCACTCACIACCCCAACCACCT 2987 167962 CAGIGACAAAGGCTTIGCCIGIAGCICTGCCCCTTIGCCACTCACIAICCCAACCACCCT 168021 |
| ative (ggaagagaa | Ş ç | 2988 GGCTCGGCACATGAAGACTCACACAGAGAACCCTTCCGCTGTCCGCTGTCCATA 3047 |
| 166942 AAGTGAAAAGGGGAGAGTTTGGAGCCTGATCCTACCCTATGCTGATGTCTCTTCTTATGT 167001 | 3 8 | CGCCTCTGCTCATCTGGATAACCTGAAAGGCACCACGCGCGTCCACACAGAGAAAAGCC |
| | ପ୍ର : | |
| CAGGG | à 4 | 168142 CTACAAGIGCCCCTCTGCCTTATGCCTGTGGCCAATCTGGCCAACCTCAAGGCTCATGG 168201 |
| ATGAGTCTGGGGGCGGGCCGGGCACTAAGTGCGGAGAGTTGAGGAGCCAGGGGGGGG | දු දු | 3168 TCGCATCCACTCTGGTGACAAACCTTTTCGGTGTAGCCTTTGCAACTACAGCTGCAACCA 3227 |
| 167122 GTCCAGGGGGCCAGGGTGAGAGGCCAGGCCCAGCCTGCCAGCTGTGTGGGGGGCCGA 167181 2243 CAGGTGGGGGCCGTGTTGTGGGGAAGAGGGGGGGGGGGG | ۶۵ بر د | 3228 GAGTATGAACCTCAAACGTCATATGCTGCGACACACGGGCGAGAAGCCCTTCCGCTGTGC 3287 |
| CAGGTGAGGGGCCGTGTTTTTTTTTTTTTTTTTTTTTTT | ò | CACCTGCGCCTATACCACAGGCCACTGGGACACAACTACAAGGTCATCACAAAGGTCATGA |
| 2303 GGTTACTGTACTCATGCCGGCTGTGCGCTTTCGTGTCCCACTACTCGAGCCACCTGAAGC 2362 | g 8 | 168322 CACCTGCGCCTATACCACGGGCCACTGGGACAACTACAAGCGCCACCAGAAGGTGCATGG 168381 |
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRMX Plate: 70 Row: d Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: Excellent library of origin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2832 GGAGGAGGGTGAGGCCAGGCTGGGAGCTGCCATGTGTGGGGCGCTGCATGCGAGGAGAA 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regreadadaccerrececreterecerrerecerrerecerrererresarer 3071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GCATCAGCGTACCCAGGCGCGCCCCCCACTCCTCCCTGCCGACCTGTGGCTTCCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2892 GECTGGAGGGTTGCCACTGGGGGACCCCAGGGCCCTGGTGACAAAGGCTTTGCCTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 GGCTGGAGGGGTGCCAGTGGGGGCCCCAGGGCCCCAGTGACAAAGGCTTTGCCTGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2592 CTGTGCTCCACGACCAACCCGGCCTCCCAGTCCCACAGAGGAGGAGGAGGAGGAACAATGCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 ATCAGAACCACTGCCAGAGCTGCTATTCCCTTGGACCTGCGGGGCTGTGGACCAAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2352 CCACCTGAAGCGGCACATGCAGACACACAGCGGGGAGAAGCCGTTCCGCTGTGGCCGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1115.4; DB 9; Length 1461;
Pred. No. 1.2e-257;
0; Mismatches 147; Indels 44;
                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mcNA"
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/clone="InAGE:4795511"
/tissue_type="Brain, hypothalamus"
/clone_lib="NHH MGC_96"
/lab_host="bH10B"
/note="DH10B"
                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 87.2%;
Matches 1307; Conservative (
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Homo sapiens, Similar to hypothetical protein FLJ32203, clone
IMAGE:4795511, mRNA.
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                                                                        3467
                                                                                                                                                                            TCTTCATTCAGACTCACCTTGAACTAAGTTCTTTTTACCTGGGGCTCTAGGAATTAG 3527
                                                                                                                                                                                                                                                                                                                                                                                 CTGGTCAGGGGCTCCACACACAGACTAACCTAGGCACTATATGGACCAGCCTGAATCCCATG 3647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGATTAGGGCCTTGGATTCACCGCCACTGCTCCCAGAGGCTATGGATGAACTGGTTGGGA 3765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA

WIN-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki

CDNA Library Arrayed by: The I M.A.G.E. Consortium (LINL)

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1461)

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Submitted (19-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
168585 CTGGCCAGGGGCTCCACACACAGACTAAGGCACTATAAGGACCAGCCCAATGG
                                                                           CCCACCCTCTGTTTTGAGCACTCGGGGTCCAGCAGCCCTGGGTGCTACTGGTAGCAGGGC
                                                                                                                                                                                                                                                                             3528 CCCTATGCCTCCTGCATTTTATACAAATGAACTAGAAACCACCTTTCCCTTTCTCCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3648 GTCAGGGGG-CCATATAGACCAGGGGA-CTTGTCTTAGCTCACGTACCAGATGAGCTAAG
                                                                                                                                                                                                                               168502 TGTCCACACACACTCATCCTGAAC---------
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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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COMMENT
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| 721 GAAACGGCACCAGCGTCCAIACAGGAGAGACCCTACAAGTGCCCCTTGCCCTTA 780 3132 TGCTGTGGCAACTGGCCAACCTCAAGGGTCATGGTCGCATCCACTGGTGACAAACC 3191 781 TGCTGTGGCAATTGGCCAACCTCAAGGGTCATGGTCCATCCA | | 3252 GCTGCGACACACGGGCGAGAAGCCCTTCCGCTGTGCCACCTGCGCCTATACCACAGGCCA 3311 901 GCTGCGGCACACGGGAGAAGCCCTTCCGCTGTGCCACCTGCGGCCTATACCACGGGCCA 960 | 3312 CTGGGACAACTACAAAGCGTCATCAGAAGGTGCATGGCCATGGTGGAGCAGGAGCGCGTGG 3371 | 3372 TCTCTGCCCCTGAGGGCTGGGCCCCACCTCATAGCCCACCCTCTGTTTTGAGCACTCG 3431 1021 TCTCTCTGCCTGAGGGCTGGGCCCACCTCATAGCCCACCTCTGTTTTGAGCTCTCG 1080 | 3432 GGGTCCAGCACCCTGGGTGCTACTAGGTAGCAGGGCTCTTTCATTCA | 3492 TAACTAGGITCTITACCIGGGGCICTAGGAATTAGCCCTAIGCCICCGGCATTIATATAC 3551 | 3552 AAATGAACTAGAAACCACCTTTCTCCCCCGCTGGTCAGGGGCTCCACACAGACT 3611 | 3612 AACCTAGGCACTATATGGACCAGCTGATCCCATGGTCAGGGGGCC-ATATAGACCAGG 3670 1224 AACGTAGGCACTATAAGGACCAGCCCAACCCATGGGCGGGGGGGCCATATGGACCAGG 1283 | 3671 GGA-CTIGICTIAGCICACGIACCAGAIGAGCIAAGIGAITAGGGCCTIGGAITCACCGC 3729 | 3730 CACTGCTCCCAGAGGCTATGGATGAACTGGTTGGGAG-CTGCCCAGCCTTTACTG 3784 | 3785 TTTTAACTTATTTCAGTGCTTTATAATAAAGGAAACACTAACAGAAAAAAAA | AX714442 N Sequence 1126 from Patent EP1293569. Sequence 1126 from Patent EP1293569. AX714442.1 G1:29889394 Homo sapiens (human) M Homo sapiens (human) M Homo sapiens (human) M Homo sapiens (human) M Homo sapiens (human) Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Ishi,S., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y. Pull-length cDNAs Patent: EP 1293569-A 1126 19-MAR-2003; Helix Research Institute (JP); Research Association for Biotechnology (JP) Incation/Qualifiers Ce |
| 3 5 5 6 | OY Pa | SP 40 | e da | 6 G | 6 G | 6 G | \rac{4}{6} | දුරු ප් | දු දු | ⊹ ය | ~ A | RESULT 15 AX714442 LOCUS LOCUS DEFINITION ACCESSION VERSION VE |

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                                                                                               Gaps
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                                                                Duery Match
29.0%; Score 1115.2; DB 6; Length 1456;
Sest Local Similarity 87.4%; Pred. No. 1.3e-257;
fatches 1305; Conservative 0; Mismatches 144; Indels 44;
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Search completed: May 14, 2004, 03:12:30 Job time : 14677 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:

May 13, 2004, 15:37:55 ; Search time 251 Seconds (without alignments) 8505.562 Million cell updates/sec

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 seqs, 277475446 residues Searched:

Total number of hits satisfying chosen parameters:

1365418

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Issued_Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | 1337, | Sequence 689, App | | | Sequence 163, App | Sequence 130, App | | Sequence 1406, Ap | Sequence 1401, Ap | Sequence 431, App | Sequence 172, App | Sequence 44, Appl | Seguence 1177, Ap | Sequence 911, App | Sequence 43, Appl | Sequence 821, App | Sequence 1054, Ap |
|-------------------|--------------------|-------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|-------------------|-------------------|--------------------|
| US-09-833-381-817 | US-09-016-434-1337 | US-09-023-655-689 | US-09-016-434-1399 | US-09-833-381-809 | US-09-620-312D-163 | US-09-220-132-130 | US-09-620-312D-586 | US-09-016-434-1406 | US-09-016-434-1401 | US-09-833-381-431 | US-09-016-434-172 | US-09-833-381-44 | US-09-833-381-1177 | US-09-620-312D-911 | US-08-676-318A-43 | US-09-833-381-821 | US-09-016-434-1054 |
| 4 | 4 | 4 | 4, | 4 | 4 | 4 | 4, | 4 | 4 | 4 | 4 | 7 | 4 | 3 | <u>س</u> | 4 | 4 |
| 890 | 2351 | 1429 | 2582 | 656 | 2925 | 1140 | 4272 | 656 | 236€ | 615 | 285 | 847 | 758 | 2038 | 543 | 1580 | 232(|
| 2.2 | 2.5 | 2.5 | 2.5 | 2.1 | 2.1 | 2.1 | 2.1 | 2.1 | 2.1 | 2.1 | 2.1 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 |
| 85.2 | 83.6 | 83.4 | 83.2 | 82.6 | 81.6 | 81.4 | 81.4 | 81.2 | 80.2 | 79.2 | 79 | 78.4 | 78 | 77.8 | 77 | 76.6 | 76.6 |
| 28 | 29 | 30 | 31 | c 35 | 33 | 34 | 35 | 36 | 37 | 38 | <u>გ</u> | c 40 | 41 | 42 | 4.3 | 44 | 45 |

ALIGNMENTS

| | Gaps 7; | TGTGGG 2733 TGTGGG 484 |
|--|--|--|
| | 1558; | ccagac ccagac |
| | Length Indels | GTTTCCTC |
| RESULT 1 UG-09-620-312D-32 Sequence 32, Application US/09620312D Patent No. 6565662 GENERAL INFORMATION: APPLICANT: 110, Chenghua APPLICANT: 110, Chenghua APPLICANT: Asundi, Vinod APPLICANT: Anang, Jie APPLICANT: Rang, Jie APPLICANT: Rang, Jie APPLICANT: Rang, Jie APPLICANT: Rang, Jie APPLICANT: Wang, Jian-hong APPLICANT: Wang, Jian-Rui APPLICANT: Wang, Donnrui APPLICANT: Wang, Wang, Mang, Wang, W | Query Match 21.2%; Score 815.2; DB 4; Best Local Similarity 85.7%; Pred. No. 1.4e-201; Matches 1004; Conservative 0; Mismatches 123; | 2674 CTGCCAGACTTGAGTCTTCATGTGCCACCAGGTGGTGCCAGTTTCCTGCCAGACTGTGGG |
| RESULTION OF CONTROL O | A Beg | \ \delta \delta \ \de |

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APPLICATION: 435
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: 304cson beg., barid A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-
TELECOMMUNICATION INFORMATION:
TELEFONE: 201-487-5800
TELEFAX: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1824 base pairs
"""" nucleic acid
                                                                                                     Sequence 1, Application US/08822701
Patent No. 5976853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ### MOLECULE TYPE: DNA (genomic)
###POTHETICAL: NO
### ANTI-SENSE: NO
US-08-822-701-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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                              1467 CAAACCGGCTGGGGGACTGCCCAGCCTCCCACTGTTAATTTAACTTATTCAGTGCTTT
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GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: All Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STREET: New Jersey
COUNTRY: USA
ZIP: 07601
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentun Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
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16.0%; Score 615.8; DB 2;
Best Local Similarity 99.7%; Pred. No. 8.8e-150;
Matches 617; Conservative 0; Mismatches 2;
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; Patent No. 6066485
; Patent No. 6066485
; GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN TILLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS;
ADDRESSE: David A. Jackson, Esq.
STREET: Ploor
STREET: Ploor
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                 373 AGCTGCTGGATCAGTGCCTGGCGCCAGACACT
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STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
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1607 TCATCGACTATCGGTTCTGTGCCTGTTGTTGTTGGAGGGAAGGACTGGTAGTTC
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APPLICANT: Gathridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
TITLE OF SEQUENCES: 22
NUMBER OF SEQUENCES: 22
ADDRESSEE: David A. Jackson, Esq.
STREET: #11 Hackensack Ave, Continental Plaza, 4th
STREET: Hackensack
CITY: Hackensack
STATE: New Jersev
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COMPOURE: Floppy disk
COMPOURE: FROM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Pred. No. 8.8e-150;
0; Mismatches 2;
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APPLICATION NUMBER: US/08/935,855
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
RAME: JACKSON ESQ., DAVIG A.
REGISTRATION NUMBER: 26,742
REPREMENS/DOCKET NUMBER: 1049-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-580
TELEPHONE: 201-343-1684
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Patent No. 6066485
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 99.7%;
Matches 617; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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: USA
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US-08-935-855-1
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Pred. No. 9.4e-150;
0; Mismatches 2; Indels 0:
                             NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAK: 201-343-1684
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 2081 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TYPE: nucleic acid
STRANDEDNES: double
TYPE: Information acid
STRANDEDNES: double
HYPOCHETICAL: NO
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Best Local Similarity 99.7%;
Matches 617; Conservative (
ATTORNEY/AGENT INFORMATION
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ORIGINAL SOURCE:
ORGANISM: Mus musculus
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RESULT 5
US-08-935-855-19
Sequence 19, Application US/08935855
Fatent No. 6066485
GENERAL INFORMATION:

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APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINJ
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, E8q.
STREET: Floor
CITY: Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CIUTRY: USA
ZIP: O'foll
COMPTRY: USA
ZIP: O'foll
COMPTRY: USA
ZIP: O'foll
COMPTRY: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURPRINT APPLICATION DATA:
PELLICATION NUMBER: US/08/935,855
FILLING DATE:
CLASSIFICATION NUMBER: US/08/935,855
FILLING DATE:
CLASSIFICATION NUMBER: US/08/935,855
FILLING DATE:
CLASSIFICATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 20.1-49-5800
TELEPHONE: 201-49-5800
TELEPHONE: 201-343-1684
NINFORMATION POR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1890 base pairs
TYPER: nucleic acid
STRANDENNESS: double
TOWNEDLY: THE COMPANDENCE CHARACTERISTICS:
LENGTH: 1890 base pairs
TYPER: NUMBERS: Gouble
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANION
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                                                                                                                                                                                                                                     Sequence 1049, Application US/09016434

Sequence 1049, Application US/09016434

Patent No. 650038

GENERAL INFORMATION:
APPLICANT: Jeffrey J. Sellhamer

APPLICANT: Jeffrey J. Sellhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE

CITY: PALO ALIFO

STATE: CALIFORNIA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 TCCGCTGCTGTACTCCACGACCAGCCCGGCCTNCCAGTCCCACAGAGCAGGA 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PErfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.4%; Score 206.2; DB 4;
92.2%; Pred. No. 6.1e-44;
tive 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 97,071
REPERENCE/DOCKET NUMBER: 97,071
RELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
786 CTIGGGCTCATCGACTATCGGTTC
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Best Local Similarity 92.2<sup>3</sup>
Matches 214; Conservative
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CLONE: 999335
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                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
TUBBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIP: 94304

COMPUTER READALE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DOWN PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
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3.0%; Score 113.8; DB 4;
Best Local Similarity 56.6%; Pred. No. 2.1e-19;
Matches 211; Conservative 0; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILING DATE: HEREWITH
CLASSIFICATION OF THE PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PILING DATE:
CLASSIFICATION NUMBER:
CLASSIFICATION NUMBER: 37,071
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 24,002 US
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1229:
SEQUENCE CHARACTERISTICS:
5-09-016-434-1229
Sequence 1229, Application US/09016434
Patent No. 6500938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2678 base pairs
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STRANDEDNESS: single
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CLONE: 9189043
US-09-016-434-1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 PORTE CITY: PALO ALTO STATE: CALIFORNIA
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3110 ACAAGTGCCCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCAACCTCAAGCGTCATGGTC 3169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.9%; Score 110.4; DB 4;
57.6%; Pred. No. 6.8e-19;
tive 0; Mismatches 146;
                                                                               3170 GCATCCACTCTGGTGACAAACCTTTTCGG
                                                                                                                                                                                                                                                                                                                                 KESGLT 9
US-09-835-381-427/c
US-09-835-381-427/c
; Sequence 427, Application US/09833381
; Series No. 6672186
; GENERAL INFORMATION:
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Patent No. 6140125
GENERAL INFORMATION:
APPLICANT: Jennifer K. Taylor
APPLICANT: Lex M. COMBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-427
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Matches 198; Conserv
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US-09-418-640-3
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      CCAGAGTATGAACCTCAAACGTCATATGCTGCGACACACGGGCGAGAAGCCCTTCCGCTG 3284
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                                                                                                                                                                                                                  Sequence 1058, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jainice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: FORMOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 2416;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/016,434 FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 111.8; DB 4;
Pred. No. 6.6e-19;
0; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                 E: INCYTE PHARMACEUTICALS, INC.
3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J. 07.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-055
INFORMATION FOR SEQ ID NO: 1058:
SEQUENCE CHARACTERISTICS:
LENGTH: 2416 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.2%;
Matches 227; Conservative (
                                                                                                                           2224 CGGTGAGTGCGGC 2236
                                                                                     3285 IGCCACCIGCGCC 3297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-09-016-434-1058
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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CACTOTGGTGACAAACCTTTTCGGTGTAGCCTTTGCAACTACAGCTGCAACCAGAGTATG
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941 AcAAGTGCAGCGCCTGCGAGAAGGCCTTCAGCTGCAGCTCGCTGCTCAGCATGCACCTGC
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TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR PRIOR PRIOR PRIOR OF SEQ ID NOS: 2000
NUMBER OF SEQ ID NOS: 2000
SOFTWARE: FaetSEQ for Windows Version 3.0
SEQ ID NO 427
LENGTH: 524
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2002 GGCAACCTCGCCAGCCACAAGACCGTCCATACCGGTGAGAAACCCTATCGTTGCAACATC 2061
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                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                       Query Match 2.6%; Score 100.4; DB 3; Length 3536; Best Local Similarity 54.3%; Pred. No. 7.4e-16; Matches 203; Conservative 0; Mismatches 171; Indels 0;
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Patent No. 5641672

GENERAL INFORMATION:

APPLICANT: Chaganti, R.S.K.

TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS

TITLE OF INVENTION: bcl-6

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: ANTISENSE MODULATION OF BCL-6 EXPRESSION
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COUNTRY:
LIL2
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTIER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: PatentIn Release #1.0, Version #1.25
                  FILE REFERENCE: RTS-0102
CURRENT APPLICATION NUMBER: US/09/418,640
CURRENT FILING DATE: 1999-10-15
CURENT FILING DATE: 89
SEQ ID NO 3
LENGTH: 3536
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STREET: 30 Rockefeller Plaza
CITY: New York
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; LOCATION: (328)..(2448)
US-09-418-640-3
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                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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US-08-074-967-1
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STATE:
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Patent No. 5882858
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dalar-Favera, Riccardo
APPLICANT: Chaganti, Raju S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bcl-6
NUMBER OF ENQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.6%; Score 100.4; DB 1; Length Best Local Similarity 54.3%; Pred. No. 7.6e-16; Matches 203; Conservative 0; Mismatches 171; Indels
                  NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/DOCKET NUMBER: 0575/43771
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 977-9550
TELEFAX: (212) 64-0525
TELEX: 4.2253 COOP UI.
SEQUENCE CHARACTERISTICS:
LENGHALION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGHH: 3720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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: United States of America
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ATTORNEY/AGENT INFORMATION:
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; LOCATION: 328..2445
US-08-074-967-1
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US-08-553-541B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.6%; Score 100.4; DB 2; Length 3720; 54.3%; Pred. No. 7.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: CAGARATI, Raju S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bcl-6
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 171; Indels
                 SOFTWARE PATENTING SITEM:

SOFTWARE PATENTING SITEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: May 28, 1996

CLASSIFICATION: 435

ATTONENY AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US

TELEFRAMICATION INFORMATION:

TELEFRAM: (212) 278-0400

TELEFRAM: (212) 278-0400

TELEFRAM: (212) 391-0525

TELEFRAM: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERESTICS:

LENGTH: 3720 base pairs

TYPE: MUCLAic acid

STRANDEDNES: double
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 1, Application US/09268202
; Patent No. 6174997
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Best Local Similarity 54.33
Matches 203; Conservative
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328..2445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-553-541B-1
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1942 CAGACCCACAGTGACAÁACCCTACAAGTGTGACCGCTGCCAGGCCTTCCTTCCGCTACAAG 2001
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GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Chaganti, R.S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bcl-6
                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Datamarible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/268,202
FILING DATE:
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                           United States of America
                                                                                                                                                                                                                                                                                                    ATTOCKEY/AGENT INFORMATION:
NAME: Wile, John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0525
TELEFAX: (212) 391-0525
TELEFAX: 422523 GOOP UI
INFORMATION FOR SED ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 3720 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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328..2445
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New York
                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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; LOCATION:
US-09-268-202-1
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PCT-US94-06669-1
                              COUNTRY:
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2980 AACCACCTGGCTCGGCACATGAAGACTCACAGTGGTGAGAAACCCTTCCGCTGTGCCCGC 3039
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                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06669
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFTCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PELLING DATE: 09-UTN-1993
ATTORNEY/AGRNT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 43771-A-PCT
REGISTRATION NUMBER: 43771-A-PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 43771-A-PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3720 base paire
IYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: double
                                                                                                                                   New York
: United States of America
                    CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2302 CATTGTGAGAGTG 2315
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LOCATION: 328..2445
NUMBER OF SEQUENCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                   CITY: New York
STATE: New Yor
                                                                                                                                                                                    10112
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
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                                                                                                                                                          COUNTRY:
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3104 AGCCCTACAAGTGCCCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCAACCTCAAGCGTC 3163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3224 ACCAGAGATATGAACCTCAAACGTCATATGCTGCGACACACGGGCGAGAAGCCCTTCCGCT 3283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3044 CATACGCCTCTGCTCATCTGGATAACCTGAAACGGCACCAGCGCGTCCACACAGAGAAA 3103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3164 ATGGTCGCATCCACTCTGGTGACAACCTTTTCGGTGTAGCCTTTGCAACTACAGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1686 GGAAGCAGTTCACCACCTCAGGGAACCTGAAGCGGCACCTTCGGATCCACAGCGGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Nauy, current APPLICANT: Wang, Tillwein APPLICANT: John Tillinghast APPLICANT: John Tillinghast APPLICANT: John Tillinghast TILE OF INVENITION: No. 656962el Nucleic Acids and TITLE OF INVENITION: No. 656962el Nucleic Acids and TITLE OF INVENITION: Polypetides FILE REPERRNCE: 784CHP2B CURRENT FILING DATE: 2000-07-19 PRIOR APPLICATION NUMBER: 09/552,317 PRIOR PILING DATE: 2000-04-25 PRIOR PILING DATE: 2000-04-25 PRIOR PILING DATE: 2000-01-21 NUMBER: OF SEQ ID NOS: 1105 SEQ ID NO 309 LE FL_Genes Version 1.0 SEQ ID NO 309 LENGTH: 2769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3284 GIGCCACCIGCGCCTATACCACAGGCCACT 3313
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                                      Sequence 309, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
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                                                                                                                                                                                            APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Xhe, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang, Yonghong
Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhou, Ping
Ma, Yunqing
Wang, Dunrui
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US-09-620-312D-309
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ORGANISM: Homo sapiens
-09-620-312D-309
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NAME/KEY: CDS
LOCATION: (248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

May 13, 2004, 22:44:48 ; Search time 1473 Seconds (without alignments) 11851.918 Million cell updates/sec

US-09-673-994A-7 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters:

2947324 seqs, 2269024515 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications Nh:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

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11: /cgn2_6/ptodata/1/pubpna/US08_EWBGOMB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/US10_EWB_FUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10_EWB_FUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10_EWB_FUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10_EWB_FUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description | Seguence 1582, Ap | Sequence 121, App | Seguence 7625, Ap | Sequence 1126, Ap | | | co, | Sequence 48, | Sequence 48, | Sequence 48, | Sequence 48, Appl | Sequence 762 | Seguence 636, App | Sequence 1, Appli |
|--------------------------|---------------------|-------------------|--------------------|--------------------|------------------|------------------|------------------|------------------|------------------|------------------|-------------------|--------------------|--------------------|-------------------|
| QI. | US-10-108-260A-1582 | US-10-221-625-121 | US-09-764-891-7625 | US-10-094-749-1126 | US-10-037-270-32 | US-10-117-722-32 | US-09-984-245-48 | US-09-966-262-48 | US-09-983-966-48 | US-10-059-395-48 | US-10-143-090-48 | US-09-764-891-7626 | US-09-917-800A-636 | US-09-813-319A-1 |
| DB | 16 | | 10 | | | | | | | | 15 | | σ | σı |
| Ouery Match Length DB | 2013 | 1975 | 9266 | | | | | | | 851 | | | 496 | |
| Query Match | 39.5 | 38.9 | 31.1 | 29.0 | 21.2 | 21.2 | 13.7 | 13.7 | 13.7 | 13.7 | 13.7 | 11.6 | 10.4 | 10.0 |
| Score | 1518 | 1498 | 1195 | 1115.2 | 815.2 | 815.2 | 528.4 | 528.4 | 528.4 | 528.4 | 528.4 | 444.8 | 399.2 | 385.6 |
| Result No. | - | 7 | m | 4 | Ŋ | v | 7 | œ | σv | 10 | 11 | 12 | (E1 |) L |

| 69, | Sequence 100, App Sequence 1049, Ap | Sequence 27851, A | Sequence 1, Appli | Sequence 5644, Ap | a) | Sequence 22, Appl | ø | | 472 | 252, | e 122 | 105 | 35, | 427, | equence | 194, | 2137 | 2300 | 231, | | 250, | e 20434, | 2538 | 196 | | 1647, | e 373, | Sequence 55, Appl | |
|------------------|--|-------------------|-------------------|-------------------|---------------------|-------------------|---------------------|---------------------|---------------|--------------------|---------------|----------------|------------------|-------------------|------------------|-------------------|---------------------|---------------------|-------------------|---------------------|-------------------|--------------|-------------|-----------|-------------------|--------------------|----------------|-------------------|------------------|
| US-10-114-893-68 | -104 | -09-918 | US-09-752-820A-1 | 4 | US-10-029-386-25436 | US-09-822-849A-22 | US-10-029-386-20893 | US-10-029-386-20288 | 10-252-157-47 | US-09-964-824A-252 | 10-305-720-12 | 10-305-720-105 | US-10-157-031-35 | US-09-833-381-427 | US-10-098-841-17 | US-10-221-625-194 | US-09-814-353-21377 | US-10-029-386-23007 | US-10-112-944-231 | US-10-108-260A-1324 | US-09-764-864-250 | 0-029-386-20 | -10-029-386 | 21-625-19 | US-10-221-625-188 | US-09-764-864-1647 | 3-10-120-988-3 | US-10-220-120-55 | US-10-034-650-24 |
| 14 | 16 | 10 | σ | σ | 15 | 0 | 12 | 15 | Ŋ | | ø | v | 15 | 6 | 14 | 13 | 10 | 15 | 13 | 16 | σ | 15 | | | | | Н | 13 | Ч |
| 1934 | 235 | 477 | 849 | 502 | 785 | 1204 | 1433 | 1458 | 2661 | 2678 | 2678 | 2416 | 2627 | 524 | 3593 | 1567 | 3614 | 1340 | 1828 | 2682 | 2131 | 1110 | 1490 | 1817 | 2032 | 3197 | 2141 | 754 | 1845 |
| 9 1 | υ ru . 4. | • | • | 3.3 | + | 9°0 | 3.0 | 3.0 | • | 3.0 | ٠. | 2.9 | | | 2.8 | | • | • | • | • | | • | • | • | • | ٠ | • | 2.7 | • |
| ~ | 206.2 | | | | 114.2 | | | 113.8 | | 113.8 | | | 111.8 | 110.4 | 108.4 | 107.8 | 106.8 | 106.6 | 106.6 | 106.6 | 106.4 | 104.8 | 104.8 | 104.8 | 104.8 | 104.8 | 102.4 | 102.2 | |
| 15 | 0 H | 18 | 13 | 20 | 21 | 22 | 23 | 24 | 52 | 26 | 27 | 28 | 5 | 30 | 31 | 32 | 33 | 34 | 32 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
| ¢ | υ | | | O | υ | O | | | | | | | | υ | | | | υ | | | | | | | | | | | |
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ALIGNMENTS

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1885 GAGGGAGATTCCACAAGCACCCTCCTCTTTAGTGGATACTGAAGATTCCTTCGACGAA 1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1945 GGTCCTGGGGCCCTGGTGTTGGAGGGGTTTGCTACTAGGCCAAGATCTGGAGTTTGAA 2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 GAGGAAGGAAGGAAGGAAGGAAGGCGACGGCAACAGTGACCAGCTCATGGGCTTCGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.5%; Score 1518; DB 16; Length 2013; Best Local Similarity 88.6%; Pred. No. 0; Matches 1727; Conservative 0; Mismatches 178; Indels 44; Gaps
                                      Sequence 1582, Application US/10108260A; Sequence 1582, Application No. US20040005560A1; Publication No. US20040005560A1; GENERAL INPORATION:
APPLICANT: PREMARTON:
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; PILE REFERENCE: H1-A0106; CURRENT APPLICATION NUMBER: US/10/108,260A; CURRENT APPLICATION NUMBER: US/10/108,260A; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: PAREITHING PARE: 2002-03-27; SOFTWARE: PAREITHIN Ver. 2.1; SOFTWARE: PAREITHIN Ver. 2.1; ENGIH: 2013
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CRGANISM: Homo sapiens
US-10-108-260A-1582
RESULT 1
US-10-108-260A-1582
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| ORGANISM: Homo sapiens FEATURE: NAME/KEX: misc_feature OTHER INFORMATION: Incyte ID No. US20040033942A1 870100CB1 -10-221-625-121 | Query Match Best Local Similarity 88.6%; Pred. No. 0; Matches 1707; Conservative 0; Mismatches 176; Indels 44; Gaps 6; | 1917 AGT(| 1977 ICH CHARGACCAAGATCTCGGAGTTTGAAGAGGAAGGG | 146 | 2037 CAACGACCAGGTCATGGGCTTTGAGAGAGACTCTGAAGGAGACTCTCAGGGGGCCAGACC 2096 | 209 CASIGACCAGALLANGGGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 266 TGGGCTTCCCTATGGGCTGAGCGACGATGAGTCTGGGGGCGGGC | 2157 GAGTGAAGTTGAGGAACCAGGGGTCCAGGGGAGGCCAGGGCTGAGAGGCCAGGCC 2216 | 2217 | 386 AGCCTGCCAGCTGTGGGGGGCCGACAGGTGAGGGCCGTGTTGTGGGGCAGGAGGGCC 44 | 2277 GGGTGGGGCCCCCGGTGCCCCCACGGTACTGTACTGCCGCGGTGTGCGCTTTCGT 23 | 446 | 233 | 5 C DOOGNETISTEED CONTRACTED CONT | 2397 CGGCTGGCGCTGCCCATACGCTTAGGCTTGGTTGGTTGGT | . 2457 C | 626 | 2517 GGGCAACCTGAGGGGGCATCAGCGCACACACAGGGCCTCCCACTCCCTCC | 2577 | 746 CIGIGGCTTCCGCTGTACTCCACGACCAGCCCCCCCCCAGTCCCAAGAGCAGGA 805 | 2637 GGGGACAATGCCCCGACGATCAGAAAATGCGCTGATCCTGCCAGACTTGAGTCTTCATGT 26 | 806 dedecenteccedecedecreaagarecrecrecrecarearricaecerecarer 86 | 2697 GCCACCAGGTGGTGCCAGTTTCCTGCCAGACTGTGGGGCAGCTGCGGGGTGAAGGGGAGAG 271 | 925 | QY 2757 CITGRGRACTGGAACCACGCCAGGCCACGCCAGGCTACTGTTCCCTTGGACCTGCCGGGG 2816 Db 926 CCTCTGCGGGACTGGAACACACACTGCCAGAGCTGCTATCCCTTGGACTGCCGGG 985 | OV 2817 CIGTGGACAGGAACTGGAGGAGGTGAGGGCAGCAGGCTGGGAAGTGCGATGTGTGGGGG 2876 | 986 |
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AGACTCACCTTGAACTAACTAGGTTCTTTTACCTGGGGCTCTAGGAATTAGCCCTATGCC 3536 GCCTCCACACACATAACGTAGGCACTATAAGGACCAACCCCATGGGCGGGGG -CCATATAGACCAGGGGA-CITGICITAGCICACGTACCAGAIGAGCTAAGTGATTAGGG CCTTGGATTCACCGCCACTGCTCCCAGAGGCTATGGATGAACTGGTTGGGAG-CTGCCCA 1646 AGACTCATCCTGAAC-----TAGGTCCTTCTT GGCTCCACACAGACTAACCTAGGCACTATATGGACCAGCCTGAATCCCATGGTCAGGGG CCCCCTCTGCCCTTATGCCTGTGGCAATCTGGCCAACCTCAAGCGTCATGGTCGCATCCA 1406 CCTCAAACGTCACATGCTGCGGCACACAGGGGAAACCCTTCCGCTGTGCCACTGCGC CIATACCACAGGCCACIGGGACAACTACAAGCGTCATCAGAAGGTGCATGGCCATGGTGG 1466 CIAIACCACGGGCCACIGGGACAACAACAAGCGCCACCAGAAGGIGCAIGGCACGGIGG 1526 GGCAGGAGGCCTGGTCTCTGAGGGCTGGGGCCCCACTCATAGCCCACTC TGTTTTGAGCACTCGGGGTCCAGCAGCCCTGGGTGCTACTGGTAGCAGGCTCTTCATTC CICTGGTGACAAACCTTTTCGGTGTAGCCTTTGCAACTACAGCTGCAACCAGATATGAA CCTCAAACGTCATATGCTGCGACACACGGGGGGGGAGAAGCCCTTCCGGCTGTGCCACCTGCGC 3357 AGCAGGAGGGCCTGGTCTCTGTGCCCCTGAGGGCTGGGGCCCCACCTCATAGCCCACCCTC TCATCTGGATAACCTGAAACGGCACCAGCGCGTCCACACAGGAAAAAGCCCTACAAGTG 1226 TCATCTGGATAACCTGAAACGGCACCAGCGCGTCCATACAGGAGAGAAGCCCTACAAGTG CCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCACCTCAAGGGTCATGGTCGCATCCA CTGCATGCGAGGAGGGCTGGAGGGGTTGCCCACTGGGGGACCCCCAGGGCCCCTGGTGACAA CATGAAGACTCACAGTGGTGAGAAACCCTTCCGCTGTGCCCGCTGTCCATACGCCTCTGC 3830 AAAAAAA 3836 AAAAAA 1975 8 6 6 6 8 8 원 수 명 ઠે S 8 8 8 8 D à 용 g ઠે g

RESULT 3 US-09-764-891-7625 ; Sequence 7625, Application US/09764891

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Best Local Similarity 81.3%; Pred. No. 0;
Matches 1568; Conservative 0; Mismatches 216; Indels 144;
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC06
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEC ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEC ID NO 7625
LENGTH: 9266
                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-7625
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 064335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT APPLICATION NUMBER: 60/350,435
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR PILING DATE: 2002-01-24
PRIOR PILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: UP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                   Sequence 1126, Application US/10094749; Publication No. US20030219741A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   APPLICANT: ISOGAL, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
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IRIE, RYCTARO
TAMBCHIKA, ICHIRO
SEKI, NACHIKO
YOSHIKAWA, ISUTOMU
OTSUKA, MOTOYUKI
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ISONO, YUUKO
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                                            3822 CTAACAGA 3829
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ORGANISM: Homo sapiens
US-10-094-749-1126
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LENGTH: 1456
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Best Local Similarity 85.7%; Pred. No. 1.6e-231;
Matches 1004; Conservative 0; Mismatches 123; Indels 45; Gaps
APPLICANT: Abang, Vinod
APPLICANT: Abang, Vinod
APPLICANT: Zhang, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
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APPLICANT: Chen, Rui-hong
APPLICANT: Webrman, Tom
APPLICANT: Wear, Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
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APPLICANT: Wang, Chiwei
APPLICANT: Wang, C
                                                                                                                                                                                       Sequence 32, Application US/10037270
Publication No. US20030104529A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Assundi, Vinod
APPLICANT: Assundi, Vinod
APPLICANT: Cheng Nei, Feiyan
APPLICANT: Chen, Rui, -hong
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ORGANISM: Homo sapiens
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; NAME/KEY: CDS
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US-10-037-270-32
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US-10-037-270-32
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3334 CAGAAGGIGCATGGCCATGGTGGAGCAGGAGCGCCTGGTCTCTCTGCCCCTCAGGGCTGG 3393
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                                                                                                                                   785 GCCGCTGTCCTTATGCCTCTGCTCATCTGGATAACCTGAAAACGGCACCAGCGCGTCCAT 844
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APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219744Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2BGIP
CURRENT APPLICATION NUMBER: US/10/117,722
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3633 1346

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3634 GCCTGAATCCCATGGTCAGGGG-CCATATAGACCAGGGGA-CTTGTCTTAGCTCACGTA 3691
                  GCCCAACCCCATGGGCGGGGGGCCCATATGGACCAGGGGACCTTGCCTTGACTGAGGCA
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Sequence 48, Application US/09984245

Patent No. US20020165374A1

GENERAL INFORMATION:
TILE REFERENCE: PZ004P1

CURRENT APPLICATION NUMBER: US/09/984,245

CURRENT APPLICATION NUMBER: US/09/984,245

CURRENT APPLICATION NUMBER: US/09/984,245

CURRENT APPLICATION NUMBER: US/09/984,245

FRICA APPLICATION NUMBER: US/09/54,707

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1997-03-21

PRIOR FILING DATE: 1997-03-21

PRIOR FILING DATE: 1997-03-21

PRIOR PELICATION NUMBER: US 60/041,276

PRIOR PELICATION NUMBER: US 60/041,276

PRIOR PELING DATE: 1997-03-21

PRIOR PELING DATE: 1997-03-21

PRIOR PELING DATE: 1997-05-30

PRIOR PELING DATE: 199
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Pred. No. 1.6e-231;
0; Mismatches 123;
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR PRILING DATE: 2000-04-25
PRIOR PLING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SEQ ID NO 32
LENGTH: 1558
                                                                                                                                                                                                                                                                                                                                                                                              21.2%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.73
Matches 1004; Conservative
                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
; FRATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1174)
US-10-117-722-32
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PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/054,804
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SOFTHARE: PALENG DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
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; Sequence 48, Application US/10059395
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Matches 701; Conservative
; LENGTH: 851
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### APPLICATION WORDER: U$ / 10.059, 395

**CURRENT FADILATION NUMBER: U$ / 10.059, 395

**CURRENT APPLICATION NUMBER: U$ / 10.059, 395

**CURRENT PLING DATE: 10.990-0.191

**RIOR PELING DATE: 10.990-0.
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| ; NUMBER OF SEQ ID NOS: 343 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 48 ; LENGTH: 851 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-143-090-48 | Query Match 13.7%; Score 528.4; DB 15; Length 851; Best Local Similarity 83.3%; Pred. No. 3.6e-146; Matches 701; Conservative 0; Mismatches 96; Indels 45; Gaps 7; | Oy 2995 CACATGAAGACTCACAGTGAGAAAACCCTTCCGCTGTGCCCGCTGTCCATACGCCTCT 3054 | Oy 3055 GCTCATCTGGATAACCTGAAACGGCACCACGCGTCCACACAGGAGAAAAGCCCTACAAG 3114 | Oy 3115 TGCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCAACCTCAAGGTCATGGTCATGTCGCATC 3174 | Oy 3175 CACTCTGGTGACAAACCTTTTCGGTGTAGCCTTTGCAACTGCAACCAGGAGTATG 3234 | Qy 3235 AACCTCAAACGTCATATGCTGCGACCACGGGGGAGAAGCCCTTCCGCTGTGCCACCTGC 3294 | Oy 3295 GCCTATACCACAGGCCACTGGGACAACTACAAGGGTCATCAGAAGGTGCATGGCCATGGT 3354 | Oy 3355 GGAGGAGGAGCCTGGTCTCTCTGCCCTGAGGGCTGGGCCCACCTCATAGCCCACCC 3414 Db 360 GGGGAGGAGAGGCCTGGTCTCTCTGCCTTGAGGGCTGGGCCCCACCTCATAGCCCACCC 419 | Db 420 TCTGTTTTGAGCACTCGGGGTCCTGGGGGCTGCTACTGGTAGCAGGGCTCTTCAT 3474 | QY 3475 TCAGACTCACCTTGAACTAACTAGGTTCTTTTACCTGGGGCTCTAGGAATTAGCCCTATG 3534 | Qy 3535 CCTCCTGCATTTTATACAAATGAACTACAACCTTTCCCTTTCTCCCCCCTGGTCA 3594 Db 510CCCATGTTTTATACAGACGACCAACGTCTTTTCTCCCCCGCTGGCCA 562 | Qy 3595 GGGGCTCCACACAGACTAACCTAGGCACTATATGGACCAGCCTGAATCCCATGGTCAGGG 3654 | 3655 GG-CCATATAGACCAGGGGA-CTTGTCTTAGCTCACGTACCAGAGGGTAAGTGATTAG 3 | 623 GGCCCATATGGACCAGGGGACCTTGCCTTGACTGAGGCACTTCACGAGCTCAGTGAGAAG | Qy 3713 GGCCTTGGATTCACCGCCACTGCTCCCAGAGGTATGAACTGGTTGGGAG-CTGCC 3771 Db 683 GGCCTTGATTCACTCCCCCAGGGGCTGTGACAAACCGGGGGACTGCC 742 Qy 3772 CAGCCTTTTAACTTAATTTCAGTGCTTTATAATAAAGGAAACACTAACA 3827 Qy 3828 GA 3829 Db 803 AA |
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| Qy 2995 CACATGAAGACTCACAGTGGAGAAACCCTTCCGCTGTGCCGCTGTCCATACGCTTCT 3054 1 CACATGAAGACTCACAGTGGTGAAGACCCTTCCGCTGCGCCGCTGTCCTTATGCTTCT 60 Qy 3055 GCTCATCTGGATAACTGGAAACGGCACCAGCGCGCTCCACAGGAGAAAAACGCTACAAG 314 Db 61 CCTCATCTGGATAACTGAAAACGGCACCAGCGCGTCCATAAGAAAAAACGCTACAAAAAAAA | 3115 | 3175 C | | OY 3295 GCCTATACCACAGGCCACTGGGACAACTACAAGGGTCATCAGAAGGTGCATGGCCATGGCT 3354 Db 300 GCCTATACCACGGGCCACTGGGACAACTACAAGCGCCACCAGAAGGTGCATGGCAGGT 359 | Oy 3355 GGAGCAGGAGGCCTGGTCTCTGCCCCTGAGGCTGGGCCCCACCTCATAGCCCACCC 3414 Db 360 GGGCAGGAGGGCCTGGTCTCTGCCTCTGAGGGCTGGGCCCACCTCATAGCCCACCC 419 | OY 3415 TCTGTTTTGAGCACTCGGGGTCCAGCAGCCCTGGGTACTGGTAGGGGGTCTTCAT 3474 Db 420 TCTGTTTTGAGCTCTCGGGGCCCACCAGCCCTGGGGACTGCTGGCAGCGGGGTGTCAC 479 | 3475 | QY 3535 CCTCCTGCATTITATACAAATGAACTAGAAACCACCTITCCCTITCTCCCCCGGTGA 3594 Db 510CCCATGTTTATACAGACGGACCAGAAGCCACCTITTITCTCCCCGGTGGCCA 562 | 2y 3595 GGGGCTCCACACACACATAAACTAAGACCAGCCTGAATCCCATGGTCAGGG 3654 Db 563 GGGGCTCCACACAGACTAACGTAGGCACTATAAGGACCAGCCCAACCCCATGGGGGGGG | OY 3655 GG-CCATATAGACCAGGGGA-CTTGTCTTAGCTCACGTACCAGATGAGTTAG 3712 | OY 3713 GGCCTTGGARTCACGGCCACTGCTCCCAGAGGCTATGGAAGTGGAACTGGTTGGAAG-CTGCC 3771 | Qy 3772 CAGCCTTTACTGTTTTAACTTGTTGCTTTATAATAAGGAAACACTAACA 3827 Db 743 CAGCCTCCCACCTGTTTATTTAACTTATTTCAGTGCTTTATAATAAGGAAACACTAACA 802 | Qy 3828 GA 3829 | Db 803 AA 804 | RESULT 11 US-10-143-090-48 US-10-143-090-48 Sequence 48, Application US/10143090 Publication No. US20030069406A1 GENERAL INFORMATION: TITLE OF INVENTION: 87 Human Secreted Proteins TITLE OF INVENTION: 87 Human Secreted Proteins TITLE REFERENCE: P2004B: 2002-05-13 CURRENT APPLICATION NUMBER: US/10/143,090 CURRENT FILING DATE: 2002-05-13 PRIOR FILING DATE: 1998-09-17 |

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Ouery Match
10.4%; Score 399.2; DB 9;
Best Local Similarity 93.0%; Pred. No. 8.5e-108;
Matches 452; Conservative 0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 636, Application US/09917800A Patent No. US20020119462A1 GENERAL INPORMATION: APPLICANT: Mendrick, Donna APPLICANT: Dorter, Mark APPLICANT: Johnson, Kory
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RESULT 12
US-09-764-891-7626

$ Sequence 7626, Application US/09764891

$ Publication No. US20330077808A1

$ GENERAL INFORMATION:

$ APPLICANT: ROSEN et al.

$ TILE OF INVENTION: Wucleic Acids, Proteins, and Antibodies

$ TURRENT PRILIG DATE: 2001-01-17

$ Prior application data removed - consult PALM or file wrapper

$ NUMBER OF SEQ ID NOS: 10231

$ SEC ID NO 7626

$ SEQ ID NO 7626

$ LENGTH: 6271
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7626
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                                                                          FEATURE:

CTHER INFORMATION: Genbank Accession No. US20020119462A1 AI058436

US-09-917-800A-636
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APPLICANT: Gatle, Arthur
APPLICANT: Blashoff, Michael
APPLICANT: Gatle, Arthur
APPLICANT: Gatle, Arthur
APPLICANT: Gatle, Michael
APPLICANT: Gene Logic, Inc.
ITILE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44221-5038-US
CURRENT PILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-10-11
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-12
PRIOR FILING DATE: 2001-05-12
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-19
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APPLICANT: ACOODS, John M.
APPLICANT: Eavallie, Edward R.
APPLICANT: Collins Racie, Lisa A.
APPLICANT: Collins Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Bowan, Michael R.
APPLICANT: Bowan, Michael R.
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Scalin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Relleher: Refired
APPLICANT: Relleher: Refired
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
PILE REPERENCE: GE 000-104
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT APPLICATION NUMBER: US/413,232
EARLIER PILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOUTHWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                  1187
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                                                              553 AC---AAAAAGAAGGCCAAGAGGGATTAGTGGTCAACCGGA-CCCTGCCCATGTGGACTG
                                                                                    CCACCCCCCCCCACGCGGCGCCTCTCTGCTGTCCTCTTAAGCCTCCTTACCTCTC
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US-10-114-893-68
US-10-114-893-68
Sequence 68, Application US/10114893
Publication No. US20020193567A1
GENERAL INFORMATION:
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; LOCATION: (24)
US-10-114-893-68
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NAME/KEY: unsure
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FEATURE:
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Sequence 1, Application US/09813319A;
Batent No. US20020108133A1
GENERAL INFORMATION:
APPLICANT: WEL, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERBNCE: CLOO1066-CIP
CURRENT APPLICATION NUMBER: US/09/813,319A
CURRENT PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-01-03
NUMBER: OF 75,820
PRIOR FILING DATE: 2001-01-03
NUMBER: OF 75,820
SEQ ID NOS: 7
SOFTWARE: PSECSE for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1435
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                                                    GAGGGAGCCTCTCCACGGAGGGGCTGAAGAATGGCAACAGTGACAAGAAGAAGCCC
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Pred. No. 1.8e-103;
0; Mismatches 69; Indels 20;
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Best Local Similarity 85.6%;
Matches 527; Conservative 0
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ORGANISM: Human
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US-09-813-319A-1
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| Gaps 8; | CAACA 432 | 24ACA 1354 | 3AGTG 492 | akdrė 1414 | CAGTG 552 | SAGCG 1474 | 3ACTG 608 | sayrd 1534 | CAGTG 667 | CAGTG 1594 | 3CCC 725 | 3Yrcr 1654 | CTCTC 785 | 3-YİC 1707 | GACTG 845 | dACTG 1763 | GCGGC 905 | GCGGC 1821 | TTTTT 965 | <u>rrrr</u> 1881 | | | |
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| Length 1934; Indels 20; | GGATGGTACAGGGTGTGA | dearderacadererea | AGTAGAGCTTCAGGCAGA | adcadadcrecadeceada | GGCTGAAGACACCGGCAA | iggcigaagaaarggcaa | -AAAAAGAAGGCCAAGAGGATTAGTGGTCAACCGGA-CCCTGCCCATGTGGACTG | cadaccccridoccacyra | CTTGTCCTTTAGCCTTAG | rrrrcrrradcrrad | -6CTGGGTGGCTTTCCTCAGCCCATTACAAAGAGGGCCCC | cegecearrecaaagage | STCCTCTTAAGCCTCCTTA | -cceedadcrividwiciccircccadccecvivre-vic | TGTTGTGTTGGAGGGAAG | -ACCGGTTCTGTGCCTGTGYTCTGTTTGGAGGGAAGGAACTG | AGGACATTCTTTTTATTG | AGGACATTYTTTTTTTTT | STACACTTTCAAGCAACACTTTTT | swacacttrcaatcaacac | | | |
| Score 376; DB 14; Pred. No. 1.6e-100; 20; Mismatches 70; | 3GCGCCAGACACTTCTGG | GCACCAGACACTTTGG | TTCAAGCCCCGAAACAC | circhaddddddaaadad | GGCACTGTCCACGGAGGG | gerecrerraereaede | GAGGGATTAGTGGTCAAC | gcgagactagcagtcard | CCGAGACTGAGTTTTGTC | CTGAGAYTGAGTTTTGTY | | GAGCTGGGTTCAM | GCCTGGGAGGCTCTGCTG | - 1 | | GGTTCTGTGCCTGTGYTC | TGTGAACACTTTATTAA | TGTGA ACTTTATTA | TGCACCGCTCTCTGTTC | recaccerryryreir | Ħ | 1897 | |
| 9.8%; nilarity 82.1%; Conservative | AGCTGCTGGATCAGTGCCTGGCGCCAGACACTTCTGGGGATGGTACAGGGTGTGA | <u>agcrigericagrectigicacaccagacacritridaggarigeracaggigidacaaca</u> | TGACGTGCATCATCATTGTTTCAAGCCCCGAAACACACAGTAGAGCTTCAGGCAGAGAGTG | reaccrecarcartrecritcaaeccceaaacacaeaeaecaecaecceaecaeaeaere | GCAAGAGGAACTGGAGGGACTGTCCACGGAGGGGCTGAAGACACCGGCAACACAGTG | gcaagcgaaaactragaggaggrgctctrractgagggggggagaaaarggcaacagcg | ACAAAAAGAAGGCCAA | acaagaagaagagagaagagagagagagagagagagaga | TTTTCTGAGCCCT-TGGACCCGAGACTGAGTTTTGTCCTTGTTCCTTTAGCCTTAGCAGTG | TTTTYTGAGCCYTCCGGACCTGAGAYTGAGTTTTGTYTTTTCCTTTAGCCTTAGCAGTG | GGTATGAGGTGTGCAGGGG | GGTATGAGGTGTGCAGGGGGAGCTGGGTTCAMTCCGCCCATTCCAAAGAGGGYTCT | CCACCCCCCACGCGGCAGCCTGGGAGCTCTGTGTCTCTTAAGCCTCTTACTCTC | cerrecacrecag | CTTGGGCTCATCGACTATCGGTTCTGTGCCTGTGCTCGTTGTGTTGGAGGGAAGGACTG | CTCGGGYTCATCACC | GTAGTTCTGATTTTTACTCTGTGAACACTTTATTTAAGGACATTCTTTTTTTAGG | GCGGTTCTGGTTTTTACTCTGTGAACTTTATTTAAGGACATTYTTTTTTTTGGCGGC | TCTGTGACCCCTAGCCGCTTGCACCCGCTCTCTGTTGTACA | tcandacictracicatracaccartritranacactricantantra | CAGACTAAAGGCCAAA 98: | cagactaaadddccaaa 18 | |
| atch cal | 373 AC | 1295 AC | 433 TC | 1355 TC | 493 G(| 1415 G | 553 A(| 1475 A(| 609 T | 1535 T | 668 G | 1595 G | 726 C | 1655 C | 786 C | 1708 C | 846 G | 1764 G | 906 T | 1822 T | 966 | 1882 C | |
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Search completed: May 14, 2004, 06:56:11 Job time : 1483 secs Н

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AI327168 CB327866 AW538698 BAS392489 AL565547 AL461955 BE908881

AW538638 BI439920

BM245850 BX672987 B1903576 B1407148 AW539472 B1950358 CA4503756 CA450376 CA8804

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May 13, 2004, 15:34:15; Search time 9218 Seconds (without alignments) 12462.552 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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AAUSZ459
Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430028M17 product:similar to CDNA FLU32203 FIS, CLONE PLACEG003038, WEALY SIMILAR TO ZINC FINGER PROTEIN 84 [Homo AKO52459.1 GI:26342688 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus Carminci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636 HTC; CAP trapper. Mus musculus (house mouse) Mus musculus RESULT 1 AK052459 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE AK052459 Mus muscu AL534516 AL534516 BQ749274 UI-M-FD0-BI668143 603295981 Description SUMMARIES AK052459 AL534516 BQ749274 BI668143

JOURNAL MEDLINE

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1247 906 735 990

21.5 19.0 18.6 17.9

827.2 732.4 716.2 687.2

DB

Length

Query Match

Score

Result No.

AL IGNMENTS

BQ208560 BI285247

AW544493 BB484959 BI407530 BD921766 BM936232 BQ1470393 BX670592 BX670592

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HGRIHSGDKPFRCSLCNYSCNQSMNLKRHMLRHTGEKPFRCATCAYTTGHWDNYKRHQ
KVHGHGGAGGPGRSAPPEGWARPPFPSVLSTRGPAALGATGSRALHSDSP"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
dev_stage="13 days embryo"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDRAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1247)
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similar to CDNA FL032203 FIS, CLONE PLACE6003038, WEAKLY
SIMILAR TO ZINC FINGER PROTEIN 84 [Homo sapiens]
(SPTM_056Mi3, evidence: FASTY, 75.2%ID, 58.9%length,
match=666)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAMTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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/mol type="mRNA"
/strain="C5TBL/64"
/db_xref="FANTOM DB:D430028M17"
/db_xref="FANTOM DB:D430028M17"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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Mus musculus (house mouse)

Mus musculus

Eukaryota; Metezoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Meteriai Rodentiai Sciurognathi; Muridae; Murinae; Mus.

Busmanialiai Eutheriai Rodentiai Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 735)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Enail: cgapba-rafmailinh.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Prayaed by: Dr. M. Bento Soares, University of Iowa CLNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
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UI-M-FDO-byf-1-07-0-UI.rl NIH_BMAP_FDO Mus musculus cDNA clone
IMAGE:5717526 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       560 CGGTGTGGCCGCTGCCCTAGGCCTCAGCTCAACCTGAACCTGACACAAACCG
                                                                                            GAGTGAAGTTGAGGAACCAGGGGTCCAGGGGAGGCCAGGGGTGAGAGGCCAGGCC
                                                                                                                                              320 cacrdaagrrcaddagccagccaggccaggccagggagggccagggcccaggccc
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TEGACITCCCIATGGGCTGAGTGACGACGAGTCTGGGGGCGGCCGCGCACTAAGTGCGGA
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/wol_type="mRNA" 606"
/dolon="CSODF004V012"
/tissue_type="FETAL BRAIN"
/dolon="Lette" Homo sapiens FETAL BRAIN"
/dolon=lib="Homo sapiens FETAL BRAIN"
/dolon=lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases I to 906)

Li,W.B., Gruber.C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Li, Don Feb 13, 2001 this sequence version replaced gi:12798009.

Contact: Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Email: seqrefagenoscope cns.fr, Web: www.genoscope.cms.fr

Library was constructed by Life Technologies, a division of

Linvitrogen. This sequence belongs to sequence cluster 1341.r For

more information about this cluster, see

http://www.genoscope.cms.fr/

cgi-bin/cluster.cgi?seq=CSODF004BB06QPIkcluster=1341.r. Contact :

Feng Liang Email: fliang@lifetech.com/URL:

Faraday Avenue Genoscope sequence ID : CSODF004BB06QPI.

Location/Qualifiers
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               1079 ATAGACCAGGGGACTTGTCTTAGCTCACGTACCAGATGAGCTAAGTGATTAGGCCTTGG
                                                                               3721 ATTCACCGCCACTGCTCCCACAGGCTATGGATCAACTGGTTGGGAGCTGCCCAGCCTTT
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                                                                                                                                                                                3781 ACTGTTTTAACTTATTTCAGTGCTTTATAATAAAGGAAACACTAACAG 3828
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 990)

28 NIH-MGC http://mgc.nci.nih.gov/

29 NIH-MGC http://mgc.nci.nih.gov/

20 Unpublished (1999)

20 Unpublished (1999)

21 Unpublished (1999)

22 Unpublished (1999)

23 Unpublished (1999)

24 Unpublished (1999)

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27 Unpublished (1999)

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603295981F1 NIH_MGC_96 Homo sapiens CDNA Clone IMAGE:5314868 5',
                                                                                                                                                                                                               661 AGGITCITITACCTGNGGCICTAGGAATTAGCCCTATGCCTCCTGCATTTTATACANATG 720
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| organism="Homo sapiens"
| ...9900
| organism="Homo sapiens"
| /mol_type="mRNA"
| /db xref="texon:9606"
| /clone="IMAGE:5314868"
| /tissue type="hypothalamus"
| /lab host="blidio"
| /lab host="blidio"
| /lab host="lab"NH-MGC_96"
| /note="lorgan: brain; vector: pBluescriptk (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (9rcga); Oligo-dr primer selected for average insert size 2:3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and primary library enriched for full-length clones and primary library enriched for full-length clones and primary library enriched for full-length clones and primary library enriched for full-length clones and primary library enriched for full-length clones and primary library constructed by M. Brownstein (MIMH/MHGRI. National Institutes of Health). Note: this:
| a NIH_MGC Library."
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                                                     3497 AGGIICITITACCIGGGCICTAGGAATTAGCCCTAIGCCICCIGCATTTTATACAAATG
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85.6%; Pred. No. 7.7e-105;
tive 0; Mismatches 129; Indels 13;
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/dev stage="embryo 12.5 dpc"
/dev stage="embryo 12.5 dpc"
/deb_nost="DH100 (TI phage resistant)"
/dlob_nost="DH100 (TI phage resistant)"
/dlob_nost="DH100 (TI phage resistant)"
/dlobe lib="NIH BMAP FD0"
/dlobe lib="NIH BMAP FD0"
/dlobe lib="In the library was constructed according to Site 2: Not I; The library was constructed according to Sold Denatured mRNa was size fractionated on a 1% agarose gel. First strand cubMA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded coDMA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is IGAGAGAGC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP); 'Gene Discovery' in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator:"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3017 AGAAACCCTTCCGCTGTGCCCGGTGTCCATACGCCTCTGCTCATCTGGATAACCTGAAAC 3076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCCCTGAGGGCTGGGCCCCACCTCATAGCCCACCTCTGTTTTGAGCACTCGGGGTC 3436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3137 GIGGCAACCIGGCCAACCICAAGCGICAIGGICGCAICCACICIGGIGACAAACCIITIC
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Best Local Similarity 99.2%; Pred. No. 1.2e-109;
Matches 729; Conservative 0; Mismatches 5;
                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                    db xref="taxon:10090"
                                                                                                                                                                                                                                                                                             clone="IMAGE:5717526"
                    Seq primer: pYX-5.
Location/Qualifiers
                                                                                                                                                                         mol_type="mRNA"
strain="C57BL/6"
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/unil_type="mRNN" septem.)
/ub_xref="taxon:866"
/clone="unkARE:575728"
/tissue_type="leukocyte"
/lab_host="mRNH"
/lab_host="mRH MG_118"
/clone lib="MRH                    E I (Dasses 1 to 1069)

S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

C Contact: Robert Strausberg, Ph.D.
Email: egapbe-remail.nih.gov.
Tissue Procurement: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12799 row: d column: 19
High quality sequence stop: 671.
High quality sequence stop: 671.
Location/Qualifiers
//noll+type="mailto:"
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dammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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92.1%; Pred. No. 3.8e-103;
live 0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             735; Conservative
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Best Local Si
Matches 735;
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lone="limb="NHH MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
inco ECORI/XhoI sites using the following o' adaptor:
GGCACGAG(G): Size-selected >500bp for average insert size
1: 8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2054 row: 1 column: 08
High quality sequence stop: 576.
721 TTATGCCTCTGCTCATCTGGATAACCTGAAACGGCACCAGCGGCGTCCATACAGGAGAA
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Pred. No. 1.5e-102;
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/clone="IMAGE:5809303"
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91.8%;
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Best Local Similarity
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ACCESSION

FEATURES

ORIGIN

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60207222F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4212245 5', BF533875
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.
1 '(Dases 1 to 843)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                  64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 ACCAGGTGCCAGTTTCCTGCCAGACTGTGGGCAGCTGCGGGGTGAAGGGAGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATACTGGCGAGAAGCCCTACCGTTGTCCCCACTGCCCCTTTGCCTGCAGCAGCCTGGG
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                                                                                                                                                              CCACTACTCGAGCCACCTGAAGCGGCACATGCAGACACACAGAGAGAAGAACACGTTCCG
                                                                                                                                                                                                                                                                                CTGTGGCCGCTGCCCATACGCNTCAGCCCAGTTCGTCAACCTGACGCGACATACCCGCAC
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    63;
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AUTHORS
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3047

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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/dolone="CSODF004Y012"
/tissue_type="FETAL BRAIN"
/dov_stage="fetal"
/dov_stage="fetal"
/clone=lib="Homo sapiens FETAL BRAIN"
/note="Torgan: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a Not1-olign(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX453491 BY 22-MAY-2003 BX453491 Homo sapiens CDNA clone CSODF004YC12 3-PRIME, mRNA sequence.
                                                                                                                                                                                                CGCCTCTGCTCATCTGGATAACCTGAAACGGCACCAGGGGGTCCACACAGAGAAAAGCC 3107
Homo sepiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 929)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Genoscope denoral de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1341.r For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAI009ZF12 CSOO862 2&cluster=1341.r.
Contact : Feng Liang Email : fliang@llfetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenu Genoscope sequence ID : CSOBAI009ZF12_CSOO862_2.
Location/Qualifiers
                                                                                                                                          659 regresecacardaaseacreacadregresaaaccerree--ersrececerereaa
                                                                                                                                                                                                                                116 CGCCTCTG-TCATCTGGATAACCTGAAA-GGGACCATCGCGT-CACACGAGAAAAGCC
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  In Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Library preparation: Loops the I.M.A.G.E. Consortium/Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Library Plate: LiAM9782 row: 1 column: 06
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/db.rate="taxon:10090"
/clone="INAGE:4212245"
/lab_host="DH10B (TI phage-resistant)"
/clone lib="MCI CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SAlI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/mol type="mRNA"
/strain="FVB/N"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 646)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/Linl at:
http://image.llnl.gov
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High quality sequence start: 7
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16.3%; Score 628; DB 12; Length 646;
Best Local Similarity 99.8%; Pred. No. 7e-95;
Matches 639; Conservative 0; Mismatches 0; Indels
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Homo sapiens
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
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       3666 CCAGGGGACTIGICTIAGCTCACGIACCAGAIGAGCIAAGIGATIAGGGCCTTGGATICA 3725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I. (bases 1 to 694)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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**DipUblished**(1997)*
Other ESTS: uf06c03.y1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (inf0@image.llnl.gov) for further information.
MGI:937416
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Best Local Similarity 94.84 Pred. No. 3.7e-94;
Matches 655; Conservative 0; Mismatches 35; Indels 1;
                                                                                                                                       /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH108"
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/organism="Mus musculus"
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:1510564"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW990386.1 GI:8186118
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Leguaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases: 1 to 793)
S. Int. Mac. nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAMN0572 row: i column: 03
High quality sequence stop: 750.
High quality sequence stop: 750.

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451 GCCCTGAGGGNTGGGCCCCACTTCATAGCCCCACTCTGTTTTGAGCACTCGGGGTCCA 392
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                                                                                                                                              391 GCAGCCCTGGCTACTGGTAGCAGGCTCTTCATTCAACTAGACTAG
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MEDLINE
PUBMED
COMMENT
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AUTHORS
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full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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                                                                                                                     Length
                                                                                                               16:04: Score 616.2; DB 12; Length 11arity 89:94: Pred. No. 6e-93; Conservative 0; Mismatches 74; Indels
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                                                                                                                                             Similarity
                                                                                                                                                                              Matches 716;
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AW536524/c
                                                                                                                              Query Match
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628 bp mRNA linear REST.31 AUG-2000 GO105E04-3 NIA Mouse E7.5 Embryonic Portion cDNA Library Mus musculus cDNA clone G0105E04 3', mRNA sequence.

AW536524.1 GI:7178941 EST.

ACCESSION VERSION KEYWORDS

DEFINITION

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15.0 LOUGGER OF TABLE OF THE COURTE OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE C
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/lab host="DH108"
/clone_lib="NIA Mouse_E7.5 Embryonic Portion cDNA_Library"
/clone_lib="NIA Mouse_E7.5 Embryonic Portion cDNA_Library"
/note="Vector: pSPORT1 (Gibco/BRL Life Technology);
Site_1: Sall; Site_2: Not1; Total RNAs were extracted from 6 Embryo. The double-stranded cDNA was synthesized by Gibco's kit with an Oligo (dT) primer [Not1 primer-adapter from GibcoBRL]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (basea I to 628)
I anaka T.S., Jaradat, S.A., Lim,M.K., Kargul,G.J., Wang,X.,
Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,
Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profilling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
Proce. Natl.: Acada: Sci. U.S.A., 97. (16); 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 AGCIGCIGGAICAGIGCCIGGCGCCAGACACIICIGGGAIGGIACAGGIGIGACAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
33 Cassell Drive, Suite 4000, Baltimore, MD 21224-6620, USA
Email: cdna@lgeun.grc.nia.nih.gov
Plater Gollos row: E column: 04
Seg primer: -21M3 Forward
High quality sequence stop: 628
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16.0%; Score 613.8; DB 10; Length

Best Local Similarity **$997.8*; Pred. No. 1.7e-92;

Matches 615; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .628
| organism="Max" musculus"
| mol_type="max" |
| strain="CS7BL/60"
| db_xref="niaEST:G0105E04-3"
| db_xref="caxon:10090"
| clone="G0105E04"
| sex="unknown"
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Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
embryo using a 15,000 mouse developmental cDNA microarray
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Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Gassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Bmail: cdna@lgsun.grc.nia.nih.gov
Plate: G0109 row: D column: 12
Seq primer: -21M13 Forward
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POLYA-Yes.
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Mus musculus Eukaryota, Atazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Eukaryota, Maranalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus. 1 (bases 1 to 727)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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L0931C10-3 NIA Mouse Newborn Kidney CDNA Library (Long) Mus
musculus CDNA clone NIA:L0931C10 IMAGE:30003009 3', mRNA sequence.
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                                                                                                     613 CTGAGCCCTTGGACCCGAGACTGAGTTTTGTCCTTGTCCTTTAGCCTTAGCAGTGGGTAT
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
Banis cdna@lgsun.grc.nia.nih.gov
Plate: L0931 row: C column: 10
Seq primer: -21M13 Forward
High quality sequence stop: 727
POLYA-Yes
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/clone lib="NIA Mouse CDNA project by the Laboratory of Genetics, National Institute on Aging (NIA); Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).
Double-grranded cDNAs were synthesized with an Oligo (dT)
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Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Pantano,S., Lim,M.K. and Ko,M.S.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contract: Dawood B. Dudekula
Contract: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
33 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Email: cdnaelgeun. grc.nia.nih.gov
Plate: L0801 row: D column: 02
Seg primer: -21M13 Forward
High quality sequence stop: 692
POLYA=Yes.
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16.0%; Score 613.8; DB 12; Length
Best Local Similarity 99.7%; Pred. No. 1.6e-92;
Matches 615; Conservative 0; Mismatches 2; Indels
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Query Match 16.0%; Score 613.8; DB 12; Length 727; Best Local Similarity 99.7%; Pred. No. 1.6e-92; Matches 615; Conservative 0; Mismatches 2; Indels 0; Gaps

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